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OM protein - protein search, using sw model

Run on: September 3, 2004, 15:56:54 ; Search time 78.2518 Seconds
(without alignments)
4199.299 Million cell updates/sec

Title: US-09-830-972-2
Perfect score: 5848
Sequence: 1 MEDIDQSSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRRKAD 1163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5848	100.0	1163	5	ABB81074	Abb81074 Rat neuro
2	5846	100.0	1163	3	AAY71310	Aay71310 Rat neuri
3	5840	99.9	1162	3	AAY71557	Aay71557 Rat Nogo
4	5823	99.6	1163	3	AAY71384	Aay71384 Alternati
5	4921	84.1	974	3	AAY71560	Aay71560 Rat Nogo
6	4403.5	75.3	1192	4	AAU04591	Aau04591 Human Nog
7	4403.5	75.3	1192	5	ABP68600	Abp68600 Human pan
8	4403.5	75.3	1192	6	ABR59667	Abr59667 Human Nog
9	4398.5	75.2	1192	3	AAY56967	Aay56967 Human MAG

10	4398.5	75.2	1192	4	AAB82349	Aab82349	Human	NOG
11	4398.5	75.2	1192	5	ABG30938	Abg30938	Human	Nog
12	4398.5	75.2	1192	5	ABB81078	Abb81078	Human	neu
13	4276.5	73.1	1178	3	AAY71311	Aay71311	Human	neu
14	4116	70.4	1246	4	AAU33228	Aau33228	Novel	hum
15	4023	68.8	803	3	AAY71562	Aay71562	Rat	Nogo
16	3714	63.5	737	3	AAY71386	Aay71386	Rat	Nogo
17	3699.5	63.3	746	3	AAY71391	Aay71391	Rat	Nogo
18	3651.5	62.4	736	3	AAY71398	Aay71398	Rat	Nogo
19	3630.5	62.1	732	3	AAY71399	Aay71399	Rat	Nogo
20	3494	59.7	695	3	AAY71387	Aay71387	Rat	Nogo
21	3436	58.8	684	3	AAY71394	Aay71394	Rat	Nogo
22	3385.5	57.9	983	6	ABU11573	Abu11573	Human	MDD
23	3280.5	56.1	893	3	AAY95012	Aay95012	Human	sec
24	2779	47.5	552	3	AAY71388	Aay71388	Rat	Nogo
25	2500.5	42.8	642	2	AAW58383	Aaw58383	Human	sec
26	2500.5	42.8	642	4	AAB90682	Aab90682	Human	BGl
27	2432	41.6	502	3	AAY71396	Aay71396	Rat	Nogo
28	2388	40.8	475	3	AAY71389	Aay71389	Rat	Nogo
29	2291	39.2	457	3	AAY71392	Aay71392	Rat	Nogo
30	1987	34.0	403	3	AAY71563	Aay71563	Rat	Nogo
31	1868	31.9	417	3	AAY71393	Aay71393	Rat	Nogo
32	1801	30.8	356	3	AAY71390	Aay71390	Rat	Nogo
33	1795.5	30.7	374	3	AAY71397	Aay71397	Rat	Nogo
34	1513	25.9	379	7	ADB85283	Adb85283	Rat	fooce
35	1416	24.2	361	3	AAY71385	Aay71385	Alternati	
36	1411.5	24.1	360	3	AAY71383	Aay71383	Rat	neuri
37	1411.5	24.1	360	5	ABB81076	Abb81076	Rat	neuro
38	1405.5	24.0	359	3	AAY71558	Aay71558	Rat	Nogo
39	1191	20.4	373	3	AAY53624	Aay53624	A bone	ma
40	1191	20.4	373	3	AAY56969	Aay56969	Human	MAG
41	1191	20.4	373	3	AAB24242	Aab24242	Human	Nog
42	1191	20.4	373	4	AAB82350	Aab82350	Human	NOG
43	1191	20.4	373	5	AAM47954	Aam47954	Human	RTN
44	1191	20.4	373	5	ABP68601	Abp68601	Human	pan
45	1191	20.4	373	5	ABB81079	Abb81079	Human	neu

ALIGNMENTS

RESULT 1

ABB81074

ID ABB81074 standard; protein; 1163 AA.

XX

AC ABB81074;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo-A.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;

KW central nervous system; peripheral nervous system; tranquillizer; Nogo;

KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;

KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;

KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;

KW neurotransmitter receptor; rat; receptor.

XX
 OS Rattus norvegicus.
 XX
 PN US2002072493-A1.
 XX
 PD 13-JUN-2002.
 XX
 PF 28-JUN-2001; 2001US-00893348.
 XX
 PR 19-MAY-1998; 98IL-00124500.
 PR 21-JUL-1998; 98WO-US014715.
 PR 22-DEC-1998; 98US-00218277.
 PR 19-MAY-1999; 99US-00314161.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
 PI Moalem G;
 XX
 DR WPI; 2002-607255/65.
 DR N-PSDB; ABN86600.
 XX
 PT Promoting nerve regeneration and preventing neuronal degeneration in the
 PT central/peripheral nervous system from injury/disease, comprises
 PT administering nervous system-specific activated T cells/antigen, or
 PT analogs/peptides.
 XX
 PS Example 5; Page 44-47; 93pp; English.
 XX
 CC The invention relates to promoting nerve regeneration or conferring
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the
 CC central/peripheral nervous system (NS). The method involves administering
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 CC combinations. The method is useful for promoting nerve regeneration and
 CC preventing neuronal degeneration in central/peripheral nervous system
 CC from injury/disease, where the injury is spinal cord injury, blunt
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
 CC damages caused by surgery such as tumour excision. The disease is not an
 CC autoimmune disease or neoplasm. The disease results in a degenerative
 CC process occurring in either gray or white matter or both. The disease is
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 CC disease, or lipoproteinemia. The present sequence represents the rat
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific

CC antigen
XX
SQ Sequence 1163 AA;

Query Match 100.0%; Score 5848; DB 5; Length 1163;
Best Local Similarity 100.0%; Pred. No. 3.9e-297;
Matches 1163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK 60

Qy     61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

Qy    121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETLFALP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETLFALP 180

Qy    181 AASEVPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AASEVPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240

Qy    241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSEFKGSPKGES 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSEFKGSPKGES 300

Qy    301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESVPGKEDRVVSPEKTMDIFNEMQMSVVA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESVPGKEDRVVSPEKTMDIFNEMQMSVVA 360

Qy    361 PVREEYADFKPFQAWQEVKDTYEGSRDVLAAARANVESKVDRKCLEDSELEQSLGKDSEGR 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PVREEYADFKPFQAWQEVKDTYEGSRDVLAAARANVESKVDRKCLEDSELEQSLGKDSEGR 420

Qy    421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480

Qy    481 QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540

Qy    541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600

Qy    601 LPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 LPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF 660

Qy    661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720

Qy    721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP 780
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Db      721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP 780
Qy      781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDIKESSETFSDSSPIE 840
Db      781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDIKESSETFSDSSPIE 840
Qy      841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
Db      841 IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
Qy      901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED 960
Db      901 DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED 960
Qy      961 RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020
Db      961 RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020
Qy     1021 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080
Db     1021 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080
Qy     1081 FLVDDLVDLKLFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140
Db     1081 FLVDDLVDLKLFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140
Qy     1141 NKSVDKAMAKIQAKIPGLKRKAD 1163
Db     1141 NKSVDKAMAKIQAKIPGLKRKAD 1163

```

RESULT 2

AAY71310

ID AAY71310 standard; protein; 1163 AA.

XX

AC AAY71310;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo A.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Inhibitory-site 1. .171

FT /note= "Inhibits NIH 3T3 fibroblast spreading"

FT Modified-site 30

FT /note= "Casein kinase II site"

FT	Region	31. .58
FT		/note= "Acidic region"
FT	Region	31. .57
FT		/note= "Region specifically described in claim 16"
FT	Region	172. .259
FT		/note= "This region is not essential for inhibitory activity"
FT	Modified-site	233
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	242. .244
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	291
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	295
FT		/note= "Protein kinase C (PKC) site"
FT	Misc-difference	404
FT		/note= "Encoded by TTG"
FT	Modified-site	436
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	468. .470
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	484
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	488
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	502
FT		/note= "Casein kinase II site"
FT	Inhibitory-site	542. .722
FT	Modified-site	576
FT		/note= "Casein kinase II site"
FT	Peptide	623. .640
FT		/note= "used as immunogen to generate antibody AS 472"
FT	Modified-site	626
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	694. .696
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	715
FT		/note= "Casein kinase II site"
FT	Peptide	762. .1163
FT		/note= "used as immunogen to generate antibody AS Bruna"
FT	Modified-site	784
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	821
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	850
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	855
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	863
FT		/note= "Casein kinase II site"
FT	Modified-site	868
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	893
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	912. .914
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	925. .927

FT /note= "Asn is N-glycosylated"
 FT Modified-site 954
 FT /note= "PKC and casein kinase II sites"
 FT Modified-site 956
 FT /note= "PKC and casein kinase II sites"
 FT Region 975. .1162
 FT /note= "This region is not essential for inhibitory
 FT activity"
 FT Region 976. .1163
 FT /note= "C-terminal common region found in Nogo A, B and C
 FT isoforms"
 FT Domain 988. .1023
 FT /label= Transmembrane_domain
 FT /note= "C-terminal hydrophobic region specifically
 FT described in claim 16"
 FT Modified-site 1024
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 1071. .1073
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 1073
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 1089
 FT /note= "Protein kinase C (PKC) site"
 FT Domain 1090. .1125
 FT /label= Transmembrane_domain
 FT /note= "C-terminal hydrophobic region specifically
 FT described in claim 16"
 FT Modified-site 1141. .1143
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 1143
 FT /note= "Protein kinase C (PKC) site"
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX
 PR 06-NOV-1998; 98US-0107446P.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX
 DR WPI; 2000-400052/34.
 DR N-PSDB; AAD01173.
 XX
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 PT of the central nervous system and inducing regeneration of neurons.
 XX
 PS Claim 3; Fig 2A; 122pp; English.
 XX
 CC The present sequence is a rat Nogo A protein which is a potent neural
 CC cell growth inhibitor and is free of all central nervous system (CNS)
 CC myelin material with which it is natively associated. The protein was
 CC derived from a cDNA generated by fusing R018U37-3, R1-3U21 cDNAs isolated

CC from hexanucleotides-primed rat brain stem/spinal cord library, and Oli18
CC cDNA from an oligo d(T)-primed rat oligodendrocyte library. Nogo proteins
CC and fragments displaying neurite growth inhibitory activity are used in
CC the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: The present sequence
CC designated as SEQ ID NO: 2 is stated to be the same as the sequence shown
CC in Fig. 13 (see AAY71384) of the specification. However, this sequence
CC does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However, the specification does not include sequences for
CC these SEQ ID numbers
XX
SQ Sequence 1163 AA;

Query Match 100.0%; Score 5846; DB 3; Length 1163;
Best Local Similarity 99.9%; Pred. No. 5e-297;
Matches 1162; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
|
Db 1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60

Qy 61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
|
Db 61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

Qy 121 PAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAPSTPAAPKRRGSGSVDETLFALP 180
|
Db 121 PAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAPSTPAAPKRRGSGSVDETLFALP 180

Qy 181 AASEVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
|
Db 181 AASEVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240

Qy 241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMSSFKGSPKGES 300
|
Db 241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMSSFKGSPKGES 300

Qy 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360
|
Db 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360

Qy 361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLEDLSLEQKSLGKDSEGR 420
|
Db 361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLEDLSLEQKSLGKDSEGR 420

Qy	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA	480
Db	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA	480
Qy	481	QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Db	481	QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Qy	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Db	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Qy	601	LPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Db	601	LPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Qy	661	NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	661	NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Qy	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP	780
Qy	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Qy	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Qy	901	DEVHVSDEFSENRRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED	960
Db	901	DEVHVSDEFSENRRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED	960
Qy	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Db	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Qy	1021	VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Db	1021	VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Qy	1081	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	1140
Db	1081	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	1140
Qy	1141	NKSVKDAMAKIQAKIPGLKRKAD	1163
Db	1141	NKSVKDAMAKIQAKIPGLKRKAD	1163

RESULT 3

AA71557

ID AA71557 standard; protein; 1162 AA.

XX
 AC AAY71557;
 XX
 DT 02-NOV-2000 (first entry)
 XX
 DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.
 XX
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; mutant; mutein.
 XX
 OS Rattus sp.
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX
 PR 06-NOV-1998; 98US-0107446P.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX
 DR WPI; 2000-400052/34.
 XX
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 PT of the central nervous system and inducing regeneration of neurons.
 XX
 PS Example; Page; 122pp; English.
 XX
 CC The patent relates to neurite growth inhibitor Nogo which is free of all
 CC central nervous system (CNS) myelin material with which it is natively
 CC associated. Nogo proteins and fragments displaying neurite growth
 CC inhibitory activity are used in the treatment of neoplastic disease of
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
 CC oligodendroglioma, menangioma, neuroblastoma or retinoblastoma and
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
 CC Therapeutics which promote Nogo activity can be used to treat or prevent
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
 CC used to inhibit production of Nogo protein to induce regeneration of
 CC neurons or to promote structural plasticity of the CNS in disorders where
 CC neurite growth, regeneration or maintenance are deficient or desired. The
 CC animal models can be used in diagnostic and screening methods for
 CC predisposition to disorders and to screen for or test molecules which can
 CC treat or prevent disorders or diseases of the CNS. The present sequence
 CC is a truncated form of rat Nogo A protein shown in AAY71310, which is
 CC used in the construction of mutant Nogo-A. Nogo-A is composed of His-
 CC tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were

CC used for mapping the inhibitory sites of Nogo protein. Major inhibitory
CC region was identified in the Nogo A sequence from amino acids 172-974,
CC particularly amino acids 542-722. In addition, N-terminal region 1-171
CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
CC present sequence is not given in the specification but is derived from
CC rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
CC However, the specification does not include sequences for these SEQ ID
CC numbers

XX

SQ Sequence 1162 AA;

Query Match 99.9%; Score 5840; DB 3; Length 1162;
Best Local Similarity 99.9%; Pred. No. 1e-296;
Matches 1161; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEDIDQSSLVSSSTDSPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK 60
        |||
Db      1 MEDIDQSSLVSSSTDSPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK 60

Qy     61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
        |||
Db     61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

Qy    121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETFLFALP 180
        |||
Db    121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETFLFALP 180

Qy    181 AASEVPVPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLP SLSPLSTVSFKEHGYL 240
        |||
Db    181 AASEVPVPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLP SLSPLSTVSFKEHGYL 240

Qy    241 GNLSAVSSSEG TIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGS SFGKSPKGES 300
        |||
Db    241 GNLSAVSSSEG TIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGS SFGKSPKGES 300

Qy    301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360
        |||
Db    301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360

Qy    361 PVREEYADFKPF EQAWEVKDTYEGSRDVLAA RANVESKVD RKCLED SLEQKSLGKDSEGR 420
        |||
Db    361 PVREEYADFKPF EQAWEVKDTYEGSRDVLAA RANVESKVD RKCLED SLEQKSLGKDSEGR 420

Qy    421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLEDHTSENKTDEKKIEERKA 480
        |||
Db    421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLEDHTSENKTDEKKIEERKA 480

Qy    481 QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540
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Db    481 QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540

Qy    541 NEATGTKIAYETKV D LVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600
        |||
Db    541 NEATGTKIAYETKV D LVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600

Qy    601 LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF 660
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Db	601		LPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Qy	661		NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	661		NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Qy	721		PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	721		PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Qy	781		NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	781		NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Qy	841		IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	841		IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Qy	901		DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Db	901		DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Qy	961		RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Db	961		RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Qy	1021		VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Db	1021		VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Qy	1081		FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	1140
Db	1081		FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	1140
Qy	1141		NKSVKDAMAKIQAKIPGLKRKA	1162
Db	1141		NKSVKDAMAKIQAKIPGLKRKA	1162

RESULT 4

AA71384

ID AAY71384 standard; protein; 1163 AA.

XX

AC AAY71384;

XX

DT 02-NOV-2000 (first entry)

XX

DE Alternative version of rat neurite growth inhibitor Nogo A.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening.


```

XX
OS   Rattus sp.
XX
FH   Key          Location/Qualifiers
FT   Inhibitory-site 1. .171
FT                               /note= "Inhibits NIH 3T3 fibroblast spreading"
FT   Modified-site   30
FT                               /note= "Casein kinase II site"
FT   Region          31. .58
FT                               /note= "Acidic region"
FT   Region          172. .259
FT                               /note= "This region is not essential for inhibitory
FT                               activity"
FT   Misc-difference 223
FT                               /label= Unknown
FT                               /note= "There is Leu at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   233
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   242. .244
FT                               /note= "Asn is N-glycosylated"
FT   Modified-site   291
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   295
FT                               /note= "Protein kinase C (PKC) site"
FT   Misc-difference 404
FT                               /note= "There is Ile at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   436
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   468. .470
FT                               /note= "Asn is N-glycosylated"
FT   Misc-difference 469
FT                               /label= Unknown
FT                               /note= "There is Lys at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   484
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FT   Modified-site   488
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   502
FT                               /note= "Casein kinase II site"
FT   Inhibitory-site 542. .722
FT   Modified-site   576
FT                               /note= "Casein kinase II site"
FT   Peptide         623. .640
FT                               /note= "used as immunogen to generate antibody AS 472"
FT   Modified-site   626
FT                               /note= "Protein kinase C (PKC) site"
FT   Misc-difference 661
FT                               /note= "There is Asn at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   694. .696
FT                               /note= "Asn is N-glycosylated"
FT   Modified-site   715
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FT   Peptide         762. .1163

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FT /note= "used as immunogen to generate antibody AS Bruna"
 FT Modified-site 784
 FT /note= "Protein kinase C (PKC) site"
 FT Misc-difference 820
 FT /note= "There is Leu at this position in the sequence
 FT shown in AAY71310"
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 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 850
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 855
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 863
 FT /note= "Casein kinase II site"
 FT Modified-site 868
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 893
 FT /note= "Protein kinase C (PKC) site"
 FT Modified-site 912. .914
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 FT Modified-site 925. .927
 FT /note= "Asn is N-glycosylated"
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 FT /note= "PKC and casein kinase II sites"
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 FT /note= "This region is not essential for inhibitory
 FT activity"
 FT Region 976. .1163
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 FT isoforms"
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 FT /note= "C-terminal hydrophobic region"
 FT Modified-site 1024
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 FT Modified-site 1071. .1073
 FT /note= "Asn is N-glycosylated"
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 FT Modified-site 1089
 FT /note= "Protein kinase C (PKC) site"
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 FT /label= Transmembrane_domain
 FT /note= "C-terminal hydrophobic region"
 FT Modified-site 1141. .1143
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 1143
 FT /note= "Protein kinase C (PKC) site"
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX

PR 06-NOV-1998; 98US-0107446P.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders

PT of the central nervous system and inducing regeneration of neurons.

XX

PS Claim 3; Fig 13; 122pp; English.

XX

CC The present sequence is an alternative version of rat Nogo A protein
CC which is a potent neural cell growth inhibitor and is free of all central
CC nervous system (CNS) myelin material with which it is natively
CC associated. Nogo proteins and fragments displaying neurite growth
CC inhibitory activity are used in the treatment of neoplastic disease of
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
CC Therapeutics which promote Nogo activity can be used to treat or prevent
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
CC used to inhibit production of Nogo protein to induce regeneration of
CC neurons or to promote structural plasticity of the CNS in disorders where
CC neurite growth, regeneration or maintenance are deficient or desired. The
CC animal models can be used in diagnostic and screening methods for
CC predisposition to disorders and to screen for or test molecules which can
CC treat or prevent disorders or diseases of the CNS. Note: The present
CC sequence is an alternative version of the Nogo A sequence shown in Fig.
CC 2A (see AAY71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ
CC ID NO: 29 in disclosure of the specification. However the specification
CC does not include sequences for these SEQ ID numbers

XX

SQ Sequence 1163 AA;

Query Match 99.6%; Score 5823; DB 3; Length 1163;

Best Local Similarity 99.7%; Pred. No. 7.9e-296;

Matches 1159; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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          |||
Db      1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK 60

Qy     61 PAAGLSAAVPPAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
          |||
Db     61 PAAGLSAAVPPAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

Qy    121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRGSGSVDETIFALP 180
          |||
Db    121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRGSGSVDETIFALP 180

Qy    181 AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
          |||
```

Db	181	AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASXPSSLSTVVSFKEHGYL	240
Qy	241	GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES	300
Db	241	GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES	300
Qy	301	AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA	360
Db	301	AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA	360
Qy	361	PVREEYADFKPFQAWVEVKDITYEGSRDVLAARANVESKVDRKCLEDSEQKSLGKDSEGR	420
Db	361	PVREEYADFKPFQAWVEVKDITYEGSRDVLAARANVESKVDRKCLEDSEQKSLGKDSEGR	420
Qy	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA	480
Db	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENXTDEKKIEERKA	480
Qy	481	QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Db	481	QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Qy	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Db	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Qy	601	LPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Db	601	LPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Qy	661	NAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	661	MAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Qy	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Qy	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Qy	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Qy	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Db	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Qy	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLS	1020
Db	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLS	1020
Qy	1021	VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Db	1021	VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080

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 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1081 FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGIA 1140
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 ||||||||||||||||||
 Db 1141 NKSVKDAMAKIQAKIPGLKRKAD 1163

RESULT 5

AA71560

ID AA71560 standard; protein; 974 AA.

XX

AC AA71560;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat Nogo A protein fragment used in the construction of mutant NiAext.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menangioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; mutant; mutein.

XX

OS Rattus sp.

XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX

PF 05-NOV-1999; 99WO-US026160.

XX

PR 06-NOV-1998; 98US-0107446P.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 PT of the central nervous system and inducing regeneration of neurons.

XX

PS Example; Page; 122pp; English.

XX

CC The patent relates to neurite growth inhibitor Nogo which is free of all
 CC central nervous system (CNS) myelin material with which it is natively
 CC associated. Nogo proteins and fragments displaying neurite growth
 CC inhibitory activity are used in the treatment of neoplastic disease of
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
 CC oligodendroglioma, menangioma, neuroblastoma or retinoblastoma and

CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
 CC Therapeutics which promote Nogo activity can be used to treat or prevent
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
 CC used to inhibit production of Nogo protein to induce regeneration of
 CC neurons or to promote structural plasticity of the CNS in disorders where
 CC neurite growth, regeneration or maintenance are deficient or desired. The
 CC animal models can be used in diagnostic and screening methods for
 CC predisposition to disorders and to screen for or test molecules which can
 CC treat or prevent disorders or diseases of the CNS. The present sequence
 CC is a fragment of rat Nogo A protein shown in AAY71310, which is used in
 CC the construction of mutant NiAext. The mutant is composed of His-tag/T7-
 CC tag/vector/Nogo-A sequence aa 1-974/T7-tag. Nogo A deletion mutants were
 CC used for mapping the inhibitory sites of Nogo protein. Major inhibitory
 CC region was identified in the Nogo A sequence from amino acids 172-974,
 CC particularly amino acids 542-722. In addition, N-terminal region 1-171
 CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
 CC present sequence is not given in the specification but is derived from
 CC rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
 CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
 CC However, the specification does not include sequences for these SEQ ID
 CC numbers
 XX
 SQ Sequence 974 AA;

Query Match 84.1%; Score 4921; DB 3; Length 974;
 Best Local Similarity 99.9%; Pred. No. 8.8e-249;
 Matches 973; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEDIDQSSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEELEVLERK	60
Db	1	MEDIDQSSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEELEVLERK	60
Qy	61	PAAGLSAAAVPPAAAAPLLDSSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP	120
Db	61	PAAGLSAAAVPPAAAAPLLDSSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP	120
Qy	121	PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRGSGSVDETFLFALP	180
Db	121	PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRGSGSVDETFLFALP	180
Qy	181	AASEPVIPISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL	240
Db	181	AASEPVIPISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL	240
Qy	241	GNLSAVSSSEGTTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES	300
Db	241	GNLSAVSSSEGTTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGES	300
Qy	301	AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA	360
Db	301	AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA	360
Qy	361	PVREEYADFKPFQAEVVKDITYEGSRDVLAARANVESKVDRKCLEDSLEQKSLGKDSEGR	420
		:	
Db	361	PVREEYADFKPFQAEVVKDITYEGSRDVLAARANVESKVDRKCIEDSLEQKSLGKDSEGR	420

Qy	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA	480
Db	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA	480
Qy	481	QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Db	481	QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Qy	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Db	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Qy	601	LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Db	601	LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Qy	661	NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	661	NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Qy	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Qy	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Qy	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Qy	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIKSKSLTKEAEKKLPSDTEKED	960
Db	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIKSKSLTKEAEKKLPSDTEKED	960
Qy	961	RSLSAVLSAELSKT	974
Db	961	RSLSAVLSAELSKT	974

RESULT 6

AAU04591

ID AAU04591 standard; protein; 1192 AA.

XX

AC AAU04591;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;

KW cranial trauma; cerebral trauma; spinal cord injury; stroke;

KW demyelinating disease; multiple sclerosis; monophasic demyelination;

KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;

KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;

KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;

KW Canavan's disease; metachromatic leukodystrophy; viral infection;
 KW Krabbe's disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1054. .1119
 FT /label= Lumenal_extracellular_domain
 FT /note= "This sequence is specifically claimed"
 FT Peptide 1055. .1094
 FT /label= Pep1
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1064. .1088
 FT /label= Pep2
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1074. .1098
 FT /label= Pep3
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1084. .1108
 FT /label= Pep4
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 FT Peptide 1095. .1119
 FT /label= Pep5
 FT /note= "Receptor binding inhibitory peptide. This
 FT sequence is specifically claimed"
 XX
 PN WO200151520-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001041.
 XX
 PR 12-JAN-2000; 2000US-0175707P.
 PR 26-MAY-2000; 2000US-0207366P.
 PR 29-SEP-2000; 2000US-0236378P.
 XX
 PA (UYYA) UNIV YALE.
 XX
 PI Strittmatter SM;
 XX
 DR WPI; 2001-442138/47.
 DR N-PSDB; AAS09453.
 XX
 PT Novel Nogo receptor protein useful for identifying modulator of Nogo
 PT protein or Nogo receptor protein, which is useful for treating central
 PT nervous system disorders.
 XX
 PS Example 1; Page 101-104; 109pp; English.
 XX
 CC The sequence is the human Nogo protein, a 250kDa myelin-associated axon
 CC growth inhibitor. The invention relates to the use of the nogo receptor,
 CC nogo protein, their nucleic acids, vectors expressing them and antibodies
 CC against them, to isolate agents which block nogo receptor mediated axonal

CC growth. The agent is useful for treating a central nervous system
 CC disorder which is a result of cranial or cerebral trauma, spinal cord
 CC injury, stroke or a demyelinating disease selected from multiple
 CC sclerosis, monophasis demyelination, encephalomyelitis, multifocal
 CC leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease,
 CC pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease,
 CC Spongy degeneration, Alexander's disease, Canavan's disease,
 CC metachromatic leukodystrophy, viral infection and Krabbe's disease
 XX
 SQ Sequence 1192 AA;

Query Match 75.3%; Score 4403.5; DB 4; Length 1192;
 Best Local Similarity 75.9%; Pred. No. 1.3e-221;
 Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;

Qy 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEEELEVLERK 60
 |||:|||| ||||| ||||| ||||| ||||| |||||:|:|:|||||
 Db 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEELEVLERK 58

Qy 61 PAAGLSAAAVP--PAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
 ||||| || || |||:|:| |||||:|:|:|||||:|:| |
 Db 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVP 118

Qy 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
 ||| ||| ||||| ||||| || || |||||
 Db 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPSTPAAPKR 178

Qy 167 RG-SGSVDETLFALPAASEVPVPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
 || ||||| ||||| |||| || |||||:|:| |||||
 Db 179 RGSSGSVDETLFALPAASEVPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy 226 LSPLSTVSFKEHGYLGNLSAVSSSEGTEETLNEASKELPERATNPFVNRDLAEFSELEY 285
 ||||| ||||| ||||| | :||:| :||:|:|:| :|| :||| |||||
 Db 238 LSPLSAAAFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy 286 SEMGSSFKGSPKGESAILVENTKKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
 ||||| || |||:| | :||:|:|:|:|:| | : ||: || | |||
 Db 298 SEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQLPTALTCLKVKED 357

Qy 340 RVVSPEKTMDIFNEMQMSVAPVREEYADFKPFQAEVVKDTEGSRDLVLA---RANV 395
 ||| || | ||| :||:| ||:|||||||: ||||: | | |:| | :|:
 Db 358 EVVSSEKAKDSFNEKRVAEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy 396 ESKVDRKCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
 ||||:| |||| : |||| |:| ||||| :|| | ||||| | :|||
 Db 417 ESKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIA 476

Qy 455 ANTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
 | |||| | ||||| |||||:|||:| || ||||| |||| ||||| |:
 Db 477 TNIFPLLDPTSENKTDEKKIEEKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNL 536

Qy 514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
 |||| |:||||| ||||| ||||| |||||:||||| :|||| |||
 Db 537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL 596

Qy 574 CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVPLEAPPPVSYSIKLEPEN 633
 |||||:||||| ||||| :|||||:|| |||| |:|:| |||

Db	597	CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSSPLEA-SSVNYESIKHEPEN	655
Qy	634	PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDF	692
Db	656	PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDF	715
Qy	693	SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS	752
Db	716	SDYSEMAKVEQPVPDPHSELVEDSSPDSEPVDLFSDDSIPEVPQKQDETVMVLKESLTETS	775
Qy	753	-ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF	809
Db	776	FESMIEYENKEKLSALPPEGGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLQMEEL	835
Qy	810	NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDFPTFVSAKDDS-PKLAKEYTDLEVS	868
Db	836	STAVYSNDDLFIKAEQIRETETFSDDSSPIEIIDFPTLISSKTSFSKLAREYTDLEVS	895
Qy	869	DKSEIANIQSGADSLPCLLEPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV	926
Db	896	HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPV	955
Qy	927	SALEPQTEMGSIVKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK	986
Db	956	SALATQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK	1015
Qy	987	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1046
Db	1016	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1075
Qy	1047	YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1106
Db	1076	YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1135
Qy	1107	NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	1136	NGLTLLILALISLFSVPVIYERHOAQIDHYLGLANKNVKDAMAKIOAKIPGLKRKAE	1192

ABP68600

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XX
PF 30-JAN-2002; 2002WO-US002781.
XX
PR 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX
DR WPI; 2002-627435/67.
DR N-PSDB; ABV94680.
XX
PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
PS Claim 2; SEQ ID NO 71; 300pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1192 AA;

Query Match 75.3%; Score 4403.5; DB 5; Length 1192;
Best Local Similarity 75.9%; Pred. No. 1.3e-221;
Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;

Qy 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
|||:|||| ||||| ||||| ||||| ||||| |||||:||||:|||||
Db 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 58
Qy 61 PAAGLSAAAVP--PAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
||||||| || ||| |||:|| :| ||||| ||||| |||||: || : |
Db 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSTVP 118

Qy 116 APSLPFAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
 ||| |||| |||||||||||||||| || || ||||||||||||
 Db 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178

Qy 167 RG-SGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
 || |||||||||||||||| || || |||||:|:||||||||||||||
 Db 179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy 226 LSPLSTVSFKEHGYLGNL SAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
 ||||| ||||| ||||| | :|||:| :|||:| :| :||| |||||
 Db 238 LSPLSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy 286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
 ||||| ||| |||:| | :||:|:|:|:|:| | : ||: || | |||
 Db 298 SEMGSSFSVSPKAESAVIVANPREETIIVKNKDEEEKLVSNILHNQQELPTALTCLKVED 357

Qy 340 RVVSPEKTMDIFNEMQMSV VAPVREEYADFKPFQAWEVKDTYEGSRDVLAA-----RANV 395
 ||| || | ||| :||| ||:|||||||: ||||: | | |:||| :|:
 Db 358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy 396 ESKVDRKCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
 |||||:| | |||| : |||| |:| ||||| :|| | ||||| | :|||
 Db 417 ESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAAATESIA 476

Qy 455 ANTFPILLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
 | |||| | |||||||||||||:||||:| | || ||||||| |||| ||||| |:
 Db 477 TNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536

Qy 514 KVTEAAVSNMPEGLTPDLVQEAACESLNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
 |||| |:||||||||||||||||| |||||||:||||| :||||| |||
 Db 537 KVTEEVVANMPEGLTPDLVQEAACESLNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL 596

Qy 574 CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPVSYDSIKLEPEN 633
 |||||:||||||||||||||||| :|||||:| | |||| |:|:| | |||
 Db 597 CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN 655

Qy 634 PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDF 692
 |||||||:|:| | : | || |||||: |||:||||||||||||||||| ||:| |
 Db 656 PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDF 715

Qy 693 SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS 752
 |:|:|:| | : ||:|:|||||||:|||||||||||||:| | |:| |:|:| | | |
 Db 716 SDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETS 775

Qy 753 -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF 809
 |:| :|:| :|:| | | |||||||: |:| | | :|:| |:|:| | ||||
 Db 776 FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEEL 835

Qy 810 NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIIDEFPTFVSAKDDS-PKLAKEYTDLEVS 868
 :|:|:| | | | |:|:|:||||||||||||||| :|:| | | |:|:| | | |
 Db 836 STAVYSNDDLFIKAEQIRETETFSDDSPIEIIIDEFPTLISSKTDSEFSKLAREYTDLEVS 895

Qy 869 DKSEIANIQSGADSLPCLELPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV 926
 ||||| || |||| | | || | | || :|:| |:|:| | : | :|
 Db 896 HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPV 955

CC The invention relates to a novel nucleic acid encoding a polypeptide
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
 CC human Nogo receptor (NgR) NTLRRCT domain), or residues 27-309 of P1 with
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS
 CC domain, provided that a partial CTS domain, if present, consists of no
 CC more than the first 39 consecutive residues. The nucleic acid of the
 CC invention has neuroprotective activity. The polynucleotide may have a use
 CC in gene therapy. The nucleic acid is useful for decreasing inhibition of
 CC axonal growth by a central nervous system (CNS) neuron. The NgR
 CC polypeptide or an agent inhibits the binding of Nogo to NgR or NgR-
 CC dependent signal transduction in the central nervous system neuron may be
 CC used in treating central nervous system disease, disorder or injury, e.g.
 CC spinal cord injury. Expression of an NgR protein may be associated with
 CC inhibition of axonal regeneration following cranial, cerebral or spinal
 CC trauma, stroke or a demyelinating disease, such as multiple sclerosis,
 CC monophasic demyelination, encephalomyelitis, multifocal
 CC leukoencephalopathy, panencephalitis, or Krabbe's disease. The present
 CC sequence is used in the exemplification of the invention
 XX
 SQ Sequence 1192 AA;

Query Match 75.3%; Score 4403.5; DB 6; Length 1192;
 Best Local Similarity 75.9%; Pred. No. 1.3e-221;
 Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;

Qy	1	MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK	60
		: : :	
Db	1	MEDLDQSPVLVSS--DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK	58
Qy	61	PAAGLSAAAVP--PAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P	115
		: : : :	
Db	59	PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSSTVP	118
Qy	116	APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Db	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR	178
Qy	167	RG-SGSVDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS	225
		: :	
Db	179	RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS	237
Qy	226	LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY	285
		: : : : : :	
Db	238	LSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY	297
Qy	286	SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESVPG-----KED	339
		: : : : : : : :	
Db	298	SEMGSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKED	357
Qy	340	RVVSPEKTMDFNEMQMSVVPVREEYADFKPFQAWVEVKDTEGSRDVLAA----RANV	395
		: : : : : : :	
Db	358	EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL	416
Qy	396	ESKVDRKCLEDSLEQKSLGKDSEGRNEDASFSTPEPVKDSSRAYITCASFT-SATESTT	454
		: : : : :	
Db	417	ESKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIA	476

DE Human MAGI polypeptide.
 XX
 KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;
 KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
 KW psychiatric disorder; developmental disorder; inflammatory disorder;
 KW stroke; cytostatic; cerebroprotective; neuroprotective.
 XX
 OS Homo sapiens.
 XX
 PN WO200005364-A1.
 XX
 PD 03-FEB-2000.
 XX
 PF 21-JUL-1999; 99WO-GB002360.
 XX
 PR 22-JUL-1998; 98GB-00016024.
 PR 19-JUL-1999; 99GB-00016898.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Michalovich D, Prinjha RK;
 XX
 DR WPI; 2000-182693/16.
 DR N-PSDB; AAZ56886.
 XX
 PT Novel polypeptides related to neuroendocrine-specific proteins and
 PT polynucleotides useful for diagnosis of various diseases and for
 PT treatment of cancer and neurological disorders.
 XX
 PS Claim 2; Page 20-21; 35pp; English.
 XX
 CC The invention relates to human MAGI protein, which is similar to
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides
 CC and antibodies are useful for treating diseases, including neuropathies,
 CC spinal injury, neuronal degeneration, neuromuscular disorders,
 CC psychiatric disorders and developmental disorders, cancer, stroke and
 CC inflammatory disorders. The polynucleotide is also useful for chromosome
 CC localization and for tissue expression studies. The present sequence
 CC represents the human MAGI protein
 XX
 SQ Sequence 1192 AA;

Query Match 75.2%; Score 4398.5; DB 3; Length 1192;
 Best Local Similarity 75.9%; Pred. No. 2.3e-221;
 Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

Qy 1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
 |||:|||| |||| |||| |||| |||| ||||:||||:|||||||
 Db 1 MEDLDQSPLVSSS-DSPRRQPAPFKYQFVREPEDEE-EEEEEEDEDEDLEEEVLERK 58
 Qy 61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
 ||||| || || |||:| :| ||||| ||||| |||||: || : |
 Db 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVP 118
 Qy 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
 ||| |||| ||||| ||||| || || || ||||| |||||

Db	119	APSPLSAAAVSPSKLPEDDEPPARPPPPASVSPQAEVWTPPPAPAPAAPSTPAAPKR	178
Qy	167	RG-SGSVDETLFALPAASEPVIPISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS	225
Db	179	RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS	237
Qy	226	LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPVFNRLAEFSELEY	285
Db	238	LSPLSAAAFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY	297
Qy	286	SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED	339
Db	298	SEMGSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKED	357
Qy	340	RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAEVWVMDTYEGSRDVLAA-----RANV	395
Db	358	EVVSSEKAKDSFNEKRAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL	416
Qy	396	ESKVDKRCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSRRAYITCASFT-SATESTT	454
Db	417	ESKVDKKCFADSLEQTNHEKDSSESSNDTSTFPSTPEGIKDRPGAYITCAPFNPAATESIA	476
Qy	455	ANTFPLLEDHTSENKTDEKKIEERKAQIIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS	513
Db	477	TNIFPLLGDPTSENKTDEKKIEEKKAIIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT	536
Qy	514	KVTEAAVSNMPEGLTPDLVQEACESELNEATGTAKIAYETKVLDLVQTSIAIQESLYPTAQL	573
Db	537	KVTEEVVANMPEGLTPDLVQEACESELNEVTGTAKIAYETKMDLVQTSVEMQESLYPAAQL	596
Qy	574	CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN	633
Db	597	CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN	655
Qy	634	PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDF	692
Db	656	PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDF	715
Qy	693	SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVS	752
Db	716	SDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQVQKQDETVMVLVKESLTETS	775
Qy	753	-ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF	809
Db	776	FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEEL	835
Qy	810	NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIIDEFPTFVSAKDDS-PKLAKEYTDLEVS	868
Db	836	STAVYSNDDLFIKESKAIQIRETETFSDDSSPIEIIIDEFPTLISKTDTSFKLAKEYTDLEVS	895
Qy	869	DKSEIANIQSGADSLPCLLPCLSLFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV	926
Db	896	HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDV	955
Qy	927	SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK	986
Db	956	SALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK	1015

Qy 987 KTG VVFGASL FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRA 1046
 |||||
 Db 1016 KTG VVFGASL FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRA 1075
 Qy 1047 YLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLKFVLMWVFTYVGALF 1106
 |||||
 Db 1076 YLESEVAISEELVQKYSNSALGHVNCTIKELRRFLVDDLVDLKFVLMWVFTYVGALF 1135
 Qy 1107 NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
 |||||:||||| |||||:|||||
 Db 1136 NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 10

AAB82349

ID AAB82349 standard; protein; 1192 AA.

XX

AC AAB82349;

XX

DT 23-JUL-2001 (first entry)

XX

DE Human NOGO-A protein.

XX

KW NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;
 KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;
 KW cerebroprotective; neuroleptic; diagnosis; therapy.

XX

OS Homo sapiens.

XX

PN WO200136631-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000WO-GB004345.

XX

PR 15-NOV-1999; 99GB-00026995.

PR

24-JAN-2000; 2000GB-00001550.

XX

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Michalovich D, Prinjha R;

XX

DR WPI; 2001-343822/36.

DR

N-PSDB; AAF90324.

XX

PT New polypeptide designated NOGO-C is a splice variant of the human NOGO
 PT gene and may be useful in the treatment of neural disorders including
 PT Alzheimer's and Parkinson's diseases.

XX

PS Disclosure; Page 26-27; 25pp; English.

XX

CC The present sequence is that of human NOGO-A. NOGO-A is a previously
 CC known splice variant of the human NOGO gene on chromosome 2p21. The
 CC invention relates to a novel splice variant, NOGO-C (see AAB82348). It

CC provides NOGO-C polypeptides and polynucleotides, and methods for
 CC producing such polypeptides by recombinant techniques. Also disclosed are
 CC methods for utilising NOGO-C polypeptides and polynucleotides in the
 CC treatment of diseases including neuropathies, spinal injury, brain
 CC injury, stroke, neuronal degeneration, for example Alzheimer's disease
 CC and Parkinson's disease, neuromuscular disorders, psychiatric disorders
 CC and developmental disorders. Also provided are methods for identifying
 CC agonists and agonists for use in treating conditions associated with NOGO
 CC -C imbalance, and diagnostic assays for detecting diseases associated
 CC with inappropriate NOGO-C activity or levels
 XX
 SQ Sequence 1192 AA;

Query Match 75.2%; Score 4398.5; DB 4; Length 1192;
 Best Local Similarity 75.9%; Pred. No. 2.3e-221;
 Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

Qy	1	MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK	60
		:	
Db	1	MEDLDQSPVLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEDEDEDLEEEVLERK	58
Qy	61	PAAGLSAAAVP--PAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P	115
Db	59	PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVP	118
Qy	116	APSLPPAAAVLP SKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Db	119	APSPLSAAAVSP SKLPEDDEPPARPPPPPPASVSPQAEPVWTPAPAPAAPPSTPAAPKR	178
Qy	167	RG-SGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS	225
Db	179	RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS	237
Qy	226	LSPLSTVSFKEHGYLGNLSAVSSSEG TIEETLNEASKELPERATNPFVNRDLAEFSELEY	285
Db	238	LSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY	297
Qy	286	SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED	339
Db	298	SEMGSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKED	357
Qy	340	RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWEVKDTYEGSRDVIAA----RANV	395
Db	358	EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL	416
Qy	396	ESKVDRKCLED SLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT	454
Db	417	ESKVDDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIA	476
Qy	455	ANTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS	513
Db	477	TNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNL	536
Qy	514	KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL	573
Db	537	KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL	596

XX
 OS Homo sapiens.
 XX
 PN WO200257483-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 18-JAN-2002; 2002WO-GB000228.
 XX
 PR 18-JAN-2001; 2001GB-00001312.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Blackstock WP, Hale RS, Prinjha R, Rowley A;
 XX
 DR WPI; 2002-599722/64.
 DR N-PSDB; ABK90134.
 XX
 PT Identifying modulators of Nogo or BACE activity for treating acute
 PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
 PT providing and monitoring interaction between Nogo and BACE polypeptides.
 XX
 PS Disclosure; Page 59-62; 68pp; English.
 XX
 CC The present invention relates to a new method of identifying modulators
 CC of Nogo function or BACE activity. The method involves providing Nogo and
 CC BACE polypeptides capable of binding with each other, monitoring the
 CC interaction between these polypeptides, and determining if the test agent
 CC is a modulator of Nogo or BACE activity. The method is useful in treating
 CC acute neuronal injuries, such as spinal or head injury, stroke,
 CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,
 CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.
 CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue
 CC hypertrophy) of the central nervous system. The BACE polypeptide is
 CC useful in screening methods to identify agents that may act as modulators
 CC of BACE activity and in particular agents that may be useful in treating
 CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
 CC and the polynucleotide encoding the BACE polypeptide are useful in
 CC manufacturing a medicament for the treatment or prevention of disorders
 CC responsive to the modulation of Nogo activity, in alleviating the
 CC symptoms or improving the condition of a patient suffering from this
 CC disorder, in axon regeneration, or in preventing metastasis or spreading
 CC of a cancer. The polynucleotide may also be an essential component in
 CC assays, a probe, in recombinant protein synthesis, and in gene therapy
 CC techniques. The present amino acid sequence represents the human NogoA
 CC protein of the invention
 XX
 SQ Sequence 1192 AA;

Query Match 75.2%; Score 4398.5; DB 5; Length 1192;
 Best Local Similarity 75.9%; Pred. No. 2.3e-221;
 Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

Qy 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEDEEDEDLEEEVLERK 60
 |||:||||| ||||| ||||| ||||| ||||| |||||:||||:|||||
 Db 1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEDEDEDLEEEVLERK 58

Qy 61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
 ||||| || ||| ||:| | ||||| |||||: || : |
 Db 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVP 118

Qy 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
 ||| ||||| ||||| ||||| ||||| || || ||||| |||||
 Db 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178

Qy 167 RG-SGSVDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
 || ||||| ||||| ||||| ||| |||||:|:||||| |||||
 Db 179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy 226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
 ||||| ||||| ||||| | :||:| :|||:| :| :||| |||||
 Db 238 LSPLSAAAFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRLTEFSELEY 297

Qy 286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
 ||||| || |||:| | :||:|:|:|:|: || : ||: || | |||
 Db 298 SEMGSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQLPTALTCLKVKED 357

Qy 340 RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDLAA----RANV 395
 ||| || | ||| :|| ||:|||||||: ||||: | | |:|| :|:
 Db 358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy 396 ESKVDRKCLEDSEQSLGKDGSEGRNEDASFPSTPEPVKDSRAYITCASFT-SATESTT 454
 ||||:| |||| : |||| |:| ||||| :|| |||| | :|||
 Db 417 ESKVDKKCFADSLEQTNHEKDSSESSNDTSTFPSTPEGIKDRPGAYITCAPFNPAAATESIA 476

Qy 455 ANTFPILLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
 | |||| | ||||| |||||:||||:| || ||||| |||| | ||||| :
 Db 477 TNIFPLLGDPSTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536

Qy 514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
 |||| |:||||| ||||| ||||| ||||| ||||| :||| |||
 Db 537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL 596

Qy 574 CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN 633
 |||||:||||| ||||| :|||:| |||| |:|:| ||||
 Db 597 CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN 655

Qy 634 PPPYEEAMNVALKAL-GTKEGIKESFNAAVQETEAPYISACDLIKETKLSTEPSPDF 692
 |||||:|:| : | || ||||: ||:||||| ||||| ||:|
 Db 656 PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDF 715

Qy 693 SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS 752
 |:|:| || |: ||:| |||||:||||| ||| |:| ||:| |||||
 Db 716 SDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVKESLTETS 775

Qy 753 -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF 809
 |:| :|| :|:| | | |||||:| :|| :|| :||:| |||||
 Db 776 FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEEL 835

Qy 810 NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIIDEFPTFVSAKDDS-PKLAKEYTDLEVS 868
 :|:| |||| | || |:|:| ||||| ||||| :|:| || ||:| |||||
 Db 836 STAVYSNDDLFIKSEAQIRETETFSFSDSSPIEIIIDEFPTLISSKTDSFSLAREYTDLEVS 895

Qy	869	DKSEIANIQSGADSLPCLLEPCDLSFKNIYPK--DEVHVVSDEFSENRSSVSKASISPSNV	926
		:: : : : : :	
Db	896	HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPV	955
Qy	927	SALEPQTEMGSIVKSKSLTKEAEKKLPSTTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK	986
		: :	
Db	956	SALATQAEIESIVKPKVLVKEAEKKLPSTTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK	1015
Qy	987	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1046
Db	1016	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1075
Qy	1047	YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1106
Db	1076	YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1135
Qy	1107	NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
		: : :	
Db	1136	NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 12

ID ABB81078 standard; protein; 1192 AA.

AC ABB81078;

DT 05-NOV-2002 (first entry)

DE Human neurotransmitter receptor protein Nogo-A.

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
KW neurotransmitter receptor; human; receptor.

OS Homo sapiens.

PN US2002072493-A1.

PD 13-JUN-2002.

PF 28-JUN-2001; 2001US-00893348.

PR 19-MAY-1998; 98IL-00124500.

PR 22-DEC-1998; 98US-00218277.

XX

VV

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;

DR WPI; 2002-607255/65.

DR N-PSDB; ABN86601.
 XX
 PT Promoting nerve regeneration and preventing neuronal degeneration in the
 PT central/peripheral nervous system from injury/disease, comprises
 PT administering nervous system-specific activated T cells/antigen, or
 PT analogs/peptides.
 XX
 PS Example; Page 53-56; 93pp; English.
 XX
 CC The invention relates to promoting nerve regeneration or conferring
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the
 CC central/peripheral nervous system (NS). The method involves administering
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
 CC combinations. The method is useful for promoting nerve regeneration and
 CC preventing neuronal degeneration in central/peripheral nervous system
 CC from injury/disease, where the injury is spinal cord injury, blunt
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
 CC damages caused by surgery such as tumour excision. The disease is not an
 CC autoimmune disease or neoplasm. The disease results in a degenerative
 CC process occurring in either gray or white matter or both. The disease is
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
 CC neuropathies associated with various diseases, including but not limited
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
 CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
 CC disease, or lipoproteinemia. The present sequence represents the human
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific
 CC antigen
 XX
 SQ Sequence 1192 AA;

Query Match 75.2%; Score 4398.5; DB 5; Length 1192;
 Best Local Similarity 75.9%; Pred. No. 2.3e-221;
 Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

Qy 1 MEDIDQSSILVSSSTDSPRRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDEDEDEDELEELVLERK 60
 |||:|||| ||||| ||||| ||||| ||||| |||||:||||:|||||
 Db 1 MEDLDQSPLVSSS-DSPRRQPAPFKYQFVREPEDEE-EEEEEEEEDEDEDELEELVLERK 58
 Qy 61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
 ||||| || ||| |||:|| :| ||||| ||||| |||||: || : |
 Db 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVP 118
 Qy 116 APSLPAAAVALPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
 ||| |||| ||||| ||||| ||||| || || ||||| |||||
 Db 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPAPAPAAPPSTPAAPKR 178

Qy 167 RG-SGSVDETLFALPAASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
 || ||||| ||||| ||||| ||||| :||| ||||| ||||| |||||
 Db 179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy 226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
 ||||| ||||| ||||| | :|||:| :|||:| :| :||| |||||
 Db 238 LSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy 286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
 ||||| ||| |||:| | :||:|:|:|:| | : ||: || | |||
 Db 298 SEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKED 357

Qy 340 RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWEVKDTYEGSRDVLAA----RANV 395
 ||| || | ||| :||| ||:|||||||: ||||: | | |:||| :|:
 Db 358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy 396 ESKVDRKCLEDLSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
 ||||:| |||| : |||| |:| ||||| :|| ||||| | :|||
 Db 417 ESKVDKKCFADSLEQTNHEKDESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIA 476

Qy 455 ANTFPILLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
 | ||| | ||||| ||||:| ||| || ||||| ||| ||||| | :
 Db 477 TNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536

Qy 514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
 |||| |:||||| ||||| ||||| :||| | :||| |||
 Db 537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL 596

Qy 574 CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPVSYDSIKLEPEN 633
 ||||:||||| ||||| :|||:| |||| |:| ||| |||
 Db 597 CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN 655

Qy 634 PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDF 692
 |||||:|:| : | || ||||: ||:||||| ||||| ||:|
 Db 656 PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDF 715

Qy 693 SNYSEIAKFEKSVPEHAELVEDSSPESEFPVDFSDDSIPEVPQTQEEAVMLMKESLTEVS 752
 |:|:| || |: |:|:|||||:|||||:| || |:| |:| ||||| |
 Db 716 SDYSEMAKVEQPVPDHSSELVEDSSPDSEFPVDFSDDSIPDVPQKQDETVMVLVKESLTETS 775

Qy 753 -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF 809
 |:| :|| :|:| | | |||||: | :||| :|| |:| ||||| |||||
 Db 776 FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEEL 835

Qy 810 NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVS 868
 |:|:| ||| | || |:|:| ||||| ||||| :|:| || |:| |||||
 Db 836 STAVYSNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSDSKLAREYTDLEVS 895

Qy 869 DKSEIANIQSGADSLPCELPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV 926
 ||||| || |||| || || || || || :|| :||:| |:| | :| :|
 Db 896 HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPV 955

Qy 927 SALEPQTEMGSIKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986
 ||| | |: ||| | | ||||| ||||| ||: ||||| |||||
 Db 956 SALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK 1015

Qy 987 KTGUVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA 1046

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Db      1016 KTG VVFGASL FLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRA 1075
QY      1047 YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF 1106
Db      1076 YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF 1135
QY      1107 NGLTLLILALISLFSIPVIYERHQVQIDHYLG LANKSVKDAMAKIQAKIPGLKRKAD 1163
Db      1136 NGLTLLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAKIQAKIPGLKRKAE 1192

```

RESULT 13

AAY71311

ID AAY71311 standard; protein; 1178 AA.

XX

AC AAY71311;

XX

DT 02-NOV-2000 (first entry)

XX

DE Human neurite growth inhibitor Nogo.

XX

KW Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
KW central nervous system; neoplastic disease; antiproliferative; glioma;
KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
KW structural plasticity; screening.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
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FT	Misc-difference	187
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	188
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	189
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	190
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	221
----	-----------------	-----

FT		/label= Unknown
----	--	-----------------

FT	Misc-difference	328
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FT		/label= Unknown
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FT	Misc-difference	477
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FT		/label= Unknown
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FT	Region	977. .1012
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FT		/note= "Region specifically described in claim 16"
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FT	Region	994. .1174
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FT		/note= "Region specifically described in claim 16"
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FT	Region	1079. .1114
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FT		/note= "Region specifically described in claim 16"
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XX

PN WO200031235-A2.

XX

PD 02-JUN-2000.

XX PF 05-NOV-1999; 99WO-US026160.
XX
PR 06-NOV-1998; 98US-0107446P.
XX
PA (SCHW/) SCHWAB M E.
PA (CHEN/) CHEN M S.
XX
PI Schwab ME, Chen MS;
XX
DR WPI; 2000-400052/34.
XX
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
PT of the central nervous system and inducing regeneration of neurons.
XX
PS Claim 11; Fig 13; 122pp; English.
XX
CC The present sequence is a human Nogo protein which is a potent neural
CC cell growth inhibitor and is free of all central nervous system (CNS)
CC myelin material with which it is natively associated. The human Nogo
CC sequence was derived by aligning human expressed sequence tags (ESTs)
CC e.g. AA158636, AA333267, AA081783, AA167765, AA322918, AA092565, AA081525
CC and AA081840 with the rat Nogo sequence. Nogo proteins and fragments
CC displaying neurite growth inhibitory activity are used in the treatment
CC of neoplastic disease of the CNS e.g. glioma, glioblastoma,
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, meningioma,
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.
CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo
CC activity can be used to treat or prevent hyperproliferative or benign
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit
CC production of Nogo protein to induce regeneration of neurons or to
CC promote structural plasticity of the CNS in disorders where neurite
CC growth, regeneration or maintenance are deficient or desired. The animal
CC models can be used in diagnostic and screening methods for predisposition
CC to disorders and to screen for or test molecules which can treat or
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
CC specification. However the specification does not include sequences for
CC these SEQ ID numbers
XX
SQ Sequence 1178 AA;

Db	119	APSPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKR	178
Qy	167	RGSGSVDETLFALPAASEPVIPISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL	226
Db	179	RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXP	224
Qy	227	SPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS	286
Db	225	SPLSAAAFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS	284
Qy	287	EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR	340
Db	285	EMGSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDE	344
Qy	341	VVSPEKTMDFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA-----RANVE	396
Db	345	VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE	403
Qy	397	SKVDRKCLEDLSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTTA	455
Db	404	SKVDKCCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT	463
Qy	456	NTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLSK	514
Db	464	NIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSDCTDYVTTDNLTK	523
Qy	515	VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLC	574
Db	524	VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC	583
Qy	575	PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENP	634
Db	584	PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENP	642
Qy	635	PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDFSN	694
Db	643	PPYEEAMSVSLKVSIGIKKEIKPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSD	702
Qy	695	YSEIAKFEKSVPEHAELVEDSSPESEPVDFLSDDSIPEVPQTQEEAVMLMKESLTEVS-E	753
Db	703	YSEMAKVEQVPDPHSELVEDSSPDSEPVDLSDDSIPDVPQKQDETVMVLKESLTETSFE	762
Qy	754	TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT	811
Db	763	SMIEYENKEKLSALPPEGGKPYLESFKLSLVNTKDTLLPDEVSTLSKKEKIPLQMEELST	822
Qy	812	AIYSNDDLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVSDK	870
Db	823	AVYSNDDLFIKAEQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHK	882
Qy	871	SEIANIQSGADSLPCLLEPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA	928
Db	883	SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNKSATSKVLLLPDVSA	942
Qy	929	L-EPQTEMGSIVKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK	987

CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU33304 represent the amino acid sequences of novel human
CC secreted proteins of the invention

XX

SQ Sequence 1246 AA;

Query Match 70.4%; Score 4116; DB 4; Length 1246;
Best Local Similarity 72.0%; Pred. No. 1.4e-206;
Matches 873; Conservative 112; Mismatches 171; Indels 56; Gaps 27;

Qy 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEELEVLERK 60
| | | : | | | | | | | | | | | | | | | | | | : | | : | | | | | | | | | |
Db 42 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEELEVLERK 99

Qy 61 PAAGLSAAAVP--PAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
| | | | | | | | | | | | | | | | | | | | | | : | | : | | | | | | | | | |
Db 100 PAAGLSAAPVPTAPAAGAPLMDFGNDVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVP 159

Qy 116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 160 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 219

Qy 167 RG-SGSVDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 220 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 278

Qy 226 LSPLSTVSFKHEGYLGNL SAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 279 LSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 338

Qy 286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 339 SEMGSSFSVSPKAESAVIVANPREEIIVKNKDDEEEKLVSNILHNQQELPTALTCLKVKED 398

Qy 340 RVVSPEKTMDIFNEMQMSVAVPREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANV 395
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 399 EVVSSEKAKDSFNEKRVAEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 457

Qy 396 ESKVDRKCLED SLEQSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 458 ESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIA 517

Qy 455 ANTFFLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 518 TNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 577

Qy 514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 578 KVTEEVVANMPEGLTPDLVQEACESELNEVTGKIAYETKMDLVQTSEVMQESLYPAAQL 637

KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; mutant; mutein.
 XX
 OS Rattus sp.
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX
 PR 06-NOV-1998; 98US-0107446P.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX
 DR WPI; 2000-400052/34.
 XX
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 PT of the central nervous system and inducing regeneration of neurons.
 XX
 PS Example; Page; 122pp; English.
 XX
 CC The patent relates to neurite growth inhibitor Nogo which is free of all
 CC central nervous system (CNS) myelin material with which it is natively
 CC associated. Nogo proteins and fragments displaying neurite growth
 CC inhibitory activity are used in the treatment of neoplastic disease of
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,
 CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.
 CC Therapeutics which promote Nogo activity can be used to treat or prevent
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be
 CC used to inhibit production of Nogo protein to induce regeneration of
 CC neurons or to promote structural plasticity of the CNS in disorders where
 CC neurite growth, regeneration or maintenance are deficient or desired. The
 CC animal models can be used in diagnostic and screening methods for
 CC predisposition to disorders and to screen for or test molecules which can
 CC treat or prevent disorders or diseases of the CNS. The present sequence
 CC is a fragment of rat Nogo A protein shown in AAY71310, which is used in
 CC the construction of mutant NiG. The mutant is composed of His-tag/T7-
 CC tag/Nogo-A sequence aa 172-974/His-tag. Nogo A deletion mutants were used
 CC for mapping the inhibitory sites of Nogo protein. Major inhibitory region
 CC was identified in the Nogo A sequence from amino acids 172-974,
 CC particularly amino acids 542-722. In addition, N-terminal region 1-171
 CC was found to be inhibitory to NIH 3T3 fibroblast spreading. Note: The
 CC present sequence is not given in the specification but is derived from
 CC rat Nogo A sequence shown in AAY71310. SEQ ID numbers 35-42 are referred
 CC in claim 32 and SEQ ID NO: 29 in disclosure of the specification.
 CC However, the specification does not include sequences for these SEQ ID

CC numbers
XX
SQ Sequence 803 AA;

Query Match 68.8%; Score 4023; DB 3; Length 803;
Best Local Similarity 99.9%; Pred. No. 6e-202;
Matches 802; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	172	VDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLST	231
Db	1	VDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLST	60
Qy	232	VSFKEHGYLGNL SAVSSSEG TIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGS	291
Db	61	VSFKEHGYLGNL SAVSSSEG TIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGS	120
Qy	292	FKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTM DIF	351
Db	121	FKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTM DIF	180
Qy	352	NEMQMSVVAPVREEYADFKPFEQAW EVKDTYEGSRDVL AARANVESKVDRKCLED SLEQK	411
Db	181	NEMQMSVVAPVREEYADFKPFEQAW EVKDTYEGSRDVL AARANVESKVDRKCLED SLEQK	240
Qy	412	SLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFP LLEDHTSENKTD	471
Db	241	SLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFP LLEDHTSENKTD	300
Qy	472	EKKIEERKAQIITEKTS PKTSPN PFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDL	531
Db	301	EKKIEERKAQIITEKTS PKTSPN PFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDL	360
Qy	532	VQEACESELNEATGTKIAYETKV D LVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDI	591
Db	361	VQEACESELNEATGTKIAYETKV D LVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDI	420
Qy	592	VMEAPLNSLLPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGTK	651
Db	421	VMEAPLNSLLPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGTK	480
Qy	652	EGIKEPESFNAAVQETEAPYIS IACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAEL	711
Db	481	EGIKEPESFNAAVQETEAPYIS IACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAEL	540
Qy	712	VEDSSPESEPV DLFSDDSIPEVPQTQEEAVMLMKESL TEVSETVAQHKEERLSASPQELG	771
Db	541	VEDSSPESEPV DLFSDDSIPEVPQTQEEAVMLMKESL TEVSETVAQHKEERLSASPQELG	600
Qy	772	KPYLESFQPNLHSTKDAASNDIPTLT KKEKISLQMEEFNTAIYSNDDLSSKEDKIKESE	831
Db	601	KPYLESFQPNLHSTKDAASNDIPTLT KKEKISLQMEEFNTAIYSNDDLSSKEDKIKESE	660
Qy	832	TFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCD	891
Db	661	TFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCD	720
Qy	892	LSFKNIYPKDEVHVSDEFSEN RSSVSKASISPSNVSALEPQTEMG SIVKSKSLTKEAEKK	951

Db |||||LSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKK 780

Qy 952 LPSDTEKEDRSLSAVLSAELSKT 974

Db |||||781 LPSDTEKEDRSLSAVLSAELSKT 803

Search completed: September 3, 2004, 16:05:24
Job time : 89.2518 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 3, 2004, 16:02:30 ; Search time 22.9601 Seconds
(without alignments)
2615.013 Million cell updates/sec

Title: US-09-830-972-2
Perfect score: 5848
Sequence: 1 MEDIDQSSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRKAD 1163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	908	15.5	199	2	US-08-700-607-1	Sequence 1, Appli
2	789.5	13.5	776	2	US-08-700-607-5	Sequence 5, Appli
3	716.5	12.3	356	2	US-08-700-607-6	Sequence 6, Appli
4	685	11.7	208	2	US-08-700-607-7	Sequence 7, Appli
5	671	11.5	267	2	US-08-700-607-8	Sequence 8, Appli
6	539.5	9.2	168	4	US-09-149-476-563	Sequence 563, App
7	519	8.9	241	2	US-08-700-607-3	Sequence 3, Appli
8	302.5	5.2	8991	4	US-08-714-741-32	Sequence 32, Appl
9	288	4.9	2468	4	US-09-976-594-726	Sequence 726, App
10	286	4.9	92	4	US-09-149-476-411	Sequence 411, App
11	279.5	4.8	1786	3	US-08-973-462-8	Sequence 8, Appli

12	265.5	4.5	1780	1	US-08-769-309A-5	Sequence 5, Appli
13	265.5	4.5	1780	3	US-08-994-570-5	Sequence 5, Appli
14	265	4.5	2137	4	US-09-134-001C-4463	Sequence 4463, Ap
15	256.5	4.4	75	4	US-09-621-976-4600	Sequence 4600, Ap
16	256.5	4.4	75	4	US-09-621-976-4601	Sequence 4601, Ap
17	254.5	4.4	1596	4	US-08-978-277A-4	Sequence 4, Appli
18	233	4.0	1142	2	US-08-993-118-7	Sequence 7, Appli
19	233	4.0	1142	3	US-08-845-528C-7	Sequence 7, Appli
20	233	4.0	1142	4	US-09-066-281B-7	Sequence 7, Appli
21	233	4.0	1142	4	US-09-468-433C-7	Sequence 7, Appli
22	232.5	4.0	1805	1	US-07-853-913-2	Sequence 2, Appli
23	230	3.9	3256	4	US-09-919-172-98	Sequence 98, Appl
24	230	3.9	3256	4	US-09-976-594-22	Sequence 22, Appl
25	228	3.9	1142	3	US-09-061-709-2	Sequence 2, Appli
26	228	3.9	1142	4	US-09-899-651-2	Sequence 2, Appli
27	228	3.9	1142	4	US-09-392-714-26	Sequence 26, Appl
28	227	3.9	1270	4	US-07-757-022B-44	Sequence 44, Appl
29	227	3.9	1311	4	US-07-757-022B-42	Sequence 42, Appl
30	227	3.9	1313	4	US-07-757-022B-142	Sequence 142, App
31	227	3.9	1314	4	US-07-757-022B-50	Sequence 50, Appl
32	227	3.9	1320	4	US-07-757-022B-46	Sequence 46, Appl
33	227	3.9	1320	4	US-07-757-022B-60	Sequence 60, Appl
34	227	3.9	1354	4	US-07-757-022B-48	Sequence 48, Appl
35	227	3.9	1361	4	US-07-757-022B-40	Sequence 40, Appl
36	227	3.9	1363	4	US-07-757-022B-52	Sequence 52, Appl
37	227	3.9	1404	4	US-07-757-022B-2	Sequence 2, Appli
38	227	3.9	1404	4	US-07-757-022B-62	Sequence 62, Appl
39	225	3.8	688	3	US-09-141-047-8	Sequence 8, Appli
40	224.5	3.8	941	4	US-07-757-022B-14	Sequence 14, Appl
41	224.5	3.8	1022	4	US-07-757-022B-84	Sequence 84, Appl
42	224.5	3.8	1038	4	US-07-757-022B-74	Sequence 74, Appl
43	224.5	3.8	1049	4	US-07-757-022B-58	Sequence 58, Appl
44	224.5	3.8	1140	4	US-07-757-022B-104	Sequence 104, App
45	224.5	3.8	1346	2	US-08-635-121-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-700-607-1

; Sequence 1, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
US-08-700-607-1

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Query Match          15.5%; Score 908; DB 2; Length 199;
Best Local Similarity 96.3%; Pred. No. 1.1e-50;
Matches 184; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy  973 KTSVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 1032
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Db  9 KDKVVDLLYWDRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGI 68

Qy  1033 QAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLKLK 1092
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Db  69 QAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKLK 128

Qy  1093 AVLMMWFTYVGFALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQ 1152
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Db  129 AVLMMWFTYVGFALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQ 188

Qy  1153 AKIPGLKRKAD 1163
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Db  189 AKIPGLKRKAE 199

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RESULT 2

US-08-700-607-5

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; Sequence 5, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.

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; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5

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Query Match          13.5%; Score 789.5; DB 2; Length 776;
Best Local Similarity 31.2%; Pred. No. 3.1e-42;
Matches 243; Conservative 115; Mismatches 252; Indels 169; Gaps 28;

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Qy      487 TSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGT 546
      : | : | ||: : : : | : | || : | : | :
Db      65 SGPARGSP--VAMETASTGVAGVSSAMDHTFSTTSKDGE-----SCYTSLI----S 110

Qy      547 KIAYETKVDLVQTSEAIQ-ESLYPTAQLCPSFEEAEATPSPVLPDI--VMEAPLNS---- 599
      | | : | : : | | : | | | ||: : | |
Db      111 DICYPPOEDSTYFTGILQKENGHVITISEP---EELGTPGPSLPDVPGLIESRGLFSSDSG 167

Qy      600 --LLPSAGASVVQPSVSPLEAPPPVSY-----DSIKLEPENPPPPYEEA-----M 641
      : | : | : ||: : | : : | : : | | :
Db      168 IEMTPAESTEVNKILADPLDQMAEAYKYIDITRPEEVKHQEQHHPELEDKDLDFKNKDT 227

Qy      642 NVALKALGTKEGIKEPE-----SFNAAVQETEAPYISACDLIKETKLSTE-PSP 690
      ::::| ||::||: : : | ||| || : | : : : |
Db      228 DISIK----PEGVREPDKPAPVEGKIIKDHLLLEESTFAPYID---DLSEEQRAPQITTP 280

Qy      691 DFSNYSEIAKFEKSVPEHAELVEDSSPESEPVDLF-SDDSIPEV---PQTQEEAVMLMK 745

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Db      281 VKITLTEIE-----PSVETTTQEKTPKQDICKPSPDTPVPTVTVSEPEDDSPGSIPTP 334
Qy      746 ESLTEVSETVAQHK-----EERLSASPQELGKPYLESFQP-----NLHSTKDAASND---- 792
      | || | : | | :| :|| : | | : | | : :
Db      335 SSGTEPSAAESQGKGSISEDELITAIKEAKGLSYETAENPRPVGQLADRPEVKARSGPPT 394
Qy      793 IPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKI----- 827
      ||: | | : : : | | : : || :
Db      395 IPSPLDHEASSAESGDSEIELVSEDPM--AAEDALPSGYVSFGHVGGPPPPSPASPSIQYS 452
Qy      828 ---KESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEI-----ANIQSG 879
      :| | || | :| | || :||| : : :| | :
Db      453 ILREERAE LDS---ELIIESCDASSASEESPKREQDSPMKPSALDAIREETGVRAEER 509
Qy      880 ADSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIV 939
      | | | | || : || | | | | | | | | | |
Db      510 APSRRGLAEPG--SFLD-YPSTEPQPGPEL-----PPGDGALEPETPM---- 549
Qy      940 KSKSLTKEAEKKLPSDTEKEDRSLSAVLSAE-----LSKTSVVDLLYWRD 984
      || | : | : : : | : | : || || |
Db      550 -----LPRKPEEDSSSNQSPAATKGPGPLGPGAPPPLLFLNKQKAIDLLYWRD 597
Qy      985 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHFP 1044
      ||: ||: ||: | || || | ||: || | ||: || | || | || | || | || | || | || |
Db      598 IKQTGIVFGSFLLLFLSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHFP 657
Qy      1045 RAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGA 1104
      :||| | : :| : ||: : : |||: || || || || || || || || || || || || || || ||
Db      658 KAYLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLMWLLTYVGA 717
Qy      1105 LFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRRAD 1163
      || || || || :| :| :| :| :| :| :| || || || | : : || || || || || || ||
Db      718 LFNGLTLLLMVVSMTLPVVVYVKHQAQIDQYLGVLVRTHINAVVAKIQAKIPGAKRHAE 776

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RESULT 3

US-08-700-607-6

; Sequence 6, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

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;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/700,607
;   FILING DATE:  Filed Herewith
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Billings, Lucy J.
;   REGISTRATION NUMBER:  36,749
;   REFERENCE/DOCKET NUMBER:  PF-0114 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-855-0555
;   TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  356 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   IMMEDIATE SOURCE:
;   LIBRARY:  GenBank
;   CLONE:  307309
US-08-700-607-6

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Query Match          12.3%;  Score 716.5;  DB 2;  Length 356;
Best Local Similarity 46.1%;  Pred. No. 4.6e-38;
Matches 164;  Conservative 48;  Mismatches 89;  Indels 55;  Gaps 7;

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Qy      828 KESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEI-----ANIQSGADS 882
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Db      36 EEREAE LDS---ELIIESCDASSASEESPKEQDSDPPMKPSALDAIREETGVRAEERAPS 92

Qy      883 LPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSK 942
          |  |  ||  :  ||  |  |  |  |||:|  |
Db      93 RRGLAEPG--SFLD-YPSTEPQPGPEL-----PPGDGALEPETPM----- 129

Qy      943 SLTKEAEKKLPSDTEKEDRSLSAVLSAE-----LSKTSVVDLLYWRDIKK 987
          ||  |:  |  :  :  :  |:  :|||:|:|:
Db      130 -----LPRKPEEDSSSNQSPAATKGGPLGPGAPPPLLFLNKQKAIDLLYWRDIKQ 180

Qy      988 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAY 1047
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Db      181 TGIVFGSFLLLFLSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHPPFKAY 240

Qy      1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1107
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Db      241 LELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLMWLLTYVGALFN 300

Qy      1108 GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRRKAD 1163
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Db      301 GLTLLLMVAVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHA 356

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RESULT 4
US-08-700-607-7
; Sequence 7, Application US/08700607
; Patent No. 5858708

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Qy 1153 AKIPGLKRRKAD 1163
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Db 198 AKIPGAKRHAE 208

RESULT 5

US-08-700-607-8

; Sequence 8, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 281046

US-08-700-607-8

Query Match 11.5%; Score 671; DB 2; Length 267;
Best Local Similarity 66.3%; Pred. No. 2.5e-35;
Matches 124; Conservative 33; Mismatches 30; Indels 0; Gaps 0;

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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
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; EARLIER APPLICATION NUMBER: 60/047,500
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; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
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; EARLIER APPLICATION NUMBER: 60/043,671
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; EARLIER APPLICATION NUMBER: 60/043,674
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; EARLIER APPLICATION NUMBER: 60/056,886
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; EARLIER APPLICATION NUMBER: 60/056,889
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594

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; EARLIER APPLICATION NUMBER: 60/056,664
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; EARLIER APPLICATION NUMBER: 60/056,876
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; EARLIER APPLICATION NUMBER: 60/056,881
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          9.2%; Score 539.5; DB 4; Length 168;
Best Local Similarity 59.3%; Pred. No. 3.2e-27;
Matches 99; Conservative 36; Mismatches 31; Indels 1; Gaps 1;
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Qy      998 LLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEE 1057
      :||| ||::|| :|: ||||| ||||| ||||| ||||| ||||| :|: |||
Db      1 MLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSE 60

Qy      1058 LVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVVGALFNGLTLLILALI 1117
      | |::| :| :| : ||||| ||||| || ||: ||||| ||||| :|:
Db      61 AFHNYMNAAMVHINRALKLIIRLFLVEDLVDLSKLAVFMWLMTYVGAVFNGITLLILAE 120
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Qy 1118 SLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGL-KRKAD 1163
 :||:|::||::: ||||:|:| | : ||||:|:| |:|:|
 Db 121 LIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAQLPGIAKKKAE 167

RESULT 7

US-08-700-607-3

; Sequence 3, Application US/08700607
 ; Patent No. 5858708
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/700,607
 ; FILING DATE: Filed Herewith
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0114 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 241 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; LIBRARY: THP1NOB01
 ; CLONE: 31870

US-08-700-607-3

Query Match 8.9%; Score 519; DB 2; Length 241;
 Best Local Similarity 59.4%; Pred. No. 1.1e-25;
 Matches 95; Conservative 33; Mismatches 32; Indels 0; Gaps 0;

Qy 972 SKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1031
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Db 44 SSCAVHDLIXWRDVKKTGFEVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRIYKSV 103

Qy 1032 IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLK 1091
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Db 104 IQAVQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHINRALKLIIRLFLVEDLVDLSLK 163

Qy 1092 FAVLMWVFTTYVGALFNGLTLLILALISLFSIPVIYERHQV 1131
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Db 164 LAVFMWLMTYVGAVFNGITLLILAELLIXSVPIVYXKYKV 203

RESULT 8

US-08-714-741-32

; Sequence 32, Application US/08714741

; Patent No. 6500613

; GENERAL INFORMATION:

; APPLICANT: Briles, David E.

; APPLICANT: McDaniel, Larry S.

; APPLICANT: Swiatlo, Edwin

; APPLICANT: Yother, Janet

; APPLICANT: Crain, Marilyn J.

; APPLICANT: Hollingshead, Susan

; APPLICANT: Tart, Rebecca

; APPLICANT: Brooks-Walter, Alexis

; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,

; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,

; TITLE OF INVENTION: PORTIONS AND PRODUCTS

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Curtis, Morris & Safford, P.C.

; STREET: 530 Fifth Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version.#1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/714,741

; FILING DATE: 16-SEP-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Frommer Esq., William S.

; REGISTRATION NUMBER: 25,506

; REFERENCE/DOCKET NUMBER: 454312-2460

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 840-3333

; TELEFAX: (212) 840-0712

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8991 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: amino acid
US-08-714-741-32

Query Match 5.2%; Score 302.5; DB 4; Length 8991;
Best Local Similarity 22.1%; Pred. No. 1.6e-09;
Matches 244; Conservative 125; Mismatches 439; Indels 297; Gaps 47;

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Qy      18 PRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDEDEDELEELVLERKPAAGLSAAAVPPAAAAAP 77
      |:| || :      :|| :||: |||      | ||      |::      || | |
Db      7805 PKPAPAPQPAPAPKPEKTDDQQAEEYARRSE--EEYNRLPQQQ-----PPKAEKP 7853

Qy      78 LLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPP 137
      : | | | :|| | |      |||      || | | | | | |
Db      7854 -----APAPKPEQPVPAEXPENP-----APAPK--PAXAPQPLKPEEPAEQP 7893

Qy     138 ARPPPPPPAGASPLAEPAPSTPAAP--KRRSGSVDETFLFALPAASEPVI PSSAEKIM 195
      | |||      || |      | || | :      | :| :| | |
Db      7894 KPEKPEEPAGQ---PEPEKPDDQQAQEDYARRSGGEYNRFPPQQPPKAEK--PAPAPK-- 7946

Qy     196 DLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSF-----KEHGYLGNL SAVSS 248
      |||      | ||: | : | :|      |      | || :
Db      7947 --PEQP-----VPAPKTLKKAKLAGAKSKAATKKAELEPELEKAEAELENLLSTLD 7996

Qy     249 SEG TIEETLNEASKELPERATNPFVNRDLAEFSEL--EYSEMGSSFKGSPKGESAILVEN 306
      || :| :| || | | | : ||| | |:: :| :      ::
Db      7997 PEG---KTQDEL DKEAAEALNKKVEALPNQVSELEEEELSKLEDNLKDAETNNVEDYIKE 8053

Qy     307 TKEEVIVRSK---DKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVAPVR 363
      || | : :|      |||: : | | |:      ||      ||
Db      8054 GLEEAIA TKQAELEKTPKELDAALN--ELGPDGDEEETPPPE-----APAE 8097

Qy     364 EEYADFKPF EQAWEVKD TYEGSRDVL AARANVESKVDRKCLED--SLEQKSLGKDSEGRN 421
      : : || |:      || | | | | :| :| :| | :| :
Db      8098 QPKPE-KPAEETPAPAPKPEKSADQQA-----EEDYARRSEEEYNRLTQQQPPKAEKPAP 8151

Qy     422 EDASFPSTPEPVK DSSRAYITCASFTSA-----TESTTANTFP LLEDHT 465
      | | | | | || | | | | | | | | | | | |
Db      8152 APAPKPEQPAPA-PKSRGLATKKKLNLA EARI ELLKKLGL EPGLEKAGAGLGNLLSTLD 8210

Qy     466 SENKTDE-----KKIEERKAQI--ITEKTSPKTSNPFVLVAVQDSEADYVTTDT 511
      | || :      ||:| | : :| :| | | :| :| :|
Db      8211 PEGKTQDEL DKEAAEALNKKVEALPNQVAELEEELSKLEDN----LKDAETNHVEDYI 8265

Qy     512 LSKVTEAAVSNMPE-----GLTPDLVQE---ACESELNEATGT KIAYET--- 552
      : || : |      | || :| | |: : | | ||
Db      8266 KEGLEEAIA TKQAELEKTPKELDAALNELGPDGDEEETPAPEAPAEQPKPEKPAEETPAP 8325

Qy     553 -----KVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAP---- 596
      : | : || | | | | | :| :| | :| |
Db      8326 APKPEKSADQQAEEYARRSEEEYNRL--TQQQPPKAEKPAPAPAP-KPEQPAPAPKKKQ 8382

Qy     597 -----LNSLLPSA-----GASVVQPSVSPL EAPPPVSYDSIKLEPENPPPYEEAM 641
      |:| | | ||: : : | || :|| | | :
Db      8383 KVNLENLLSTLDPGGKTQDEL DKGAAEALNKKVEALPNPVX----ELEEELSPPEDN-- 8436

Qy     642 NVALKALGT-----KEGIKE-----PESFNAAV-----QETEAPYIS 673
      || |      |||::|      |: :||:      :|| |
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Db 8437 ---LKDAETNHVEDYIKEGLEEAIATKQAELEETPQEVDAALNDLVPDGGEEETPAP--- 8490

Qy 674 IACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAE-----LVEDSSPESE 720
 : : : |:| : | || : || | : |:|

Db 8491 ----APQPDEPAPAPAPNAEQPAPAPKPEKSADQQAEEEDYARRSEGEYNRLTQQQPPKAE 8546

Qy 721 -PVDLFSDDSIPEVPQTQEEAVML-----MKESLTVSETVAQHKEERLSASPQ 768
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Db 8547 KPAPAPAPKPEQPAPAPNKEIARLQSDLKDAEENNVEDYIKEGLEQAITNKKAEIATTTQ 8606

Qy 769 ELGKPYLESFQPNLHSTKDAASNDIPTLTKE-----KISLQMEEFNTAIYSNDDLL 820
 : | : | | |:| |:| : : :| : :|

Db 8607 NIDKTQKDLEDAELELEKVLATLDPEGKTQDELDKEAAEAELENEKVEALQNQVAEELEEL 8666

Qy 821 SSKEDKIKESETFSDSSPI-EIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSG 879
 | || :| :| : | | :| :| :| :|

Db 8667 SKLEDNLKDAETNNVEDYIKEGLEE-----AIATKKAELEKTQKE----- 8706

Qy 880 ADSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSI 939
 | : : | : :| :| :| | | |:|

Db 8707 -----LDAALNELGPDGD---EEETPAPAPQPEKPAEEPEN-PAPAPKPE----- 8747

Qy 940 KSKSLTKEAEKKLPSDTEKEDRSL 964
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Db 8748 --KSADQQAEEEDYARRSEEEYNRLT 8770

RESULT 9

US-09-976-594-726

; Sequence 726, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 726

; LENGTH: 2468

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. 6673549 4295277CD1

US-09-976-594-726

Query Match 4.9%; Score 288; DB 4; Length 2468;

Best Local Similarity 20.2%; Pred. No. 2e-09;

Matches 251; Conservative 166; Mismatches 441; Indels 386; Gaps 56;

Qy 13 STDSPPR--PPPAFKYQFVTEPEDEEEDDEE-----EED-----EEEDDED 50

	: :	:	: :: :	:			
Db	625	ATDVKPKAAKEKTVKKETKVKPEDKKEEKEKPKKEVAKKEDKTPIKKEEKPKKEEVKKEV	684				
Qy	51	LEELEVLERKPAAGLSAAAVPPAAAAPLLDfSSDSVPPAPRGPLPAAPPAAPERQPSWER	110				
		: :: :	:	:: :	:	:	
Db	685	KKEIKKEEKK-----EPKKEVKKETPPKEVKKEVKKEEKKEVKKE---EK	726				
Qy	111	SPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRG--	168				
			:	:	:	:	:
Db	727	EPKKEIKKLPKDAKKSSTPLSEAKKPAALKPKVPKKEESVKKDSVA----AGKPKEKGKI	782				
Qy	169	-----SGSVDETLFAL-----PA-----ASEPVI PSSAEKIMDLME	199				
		:	:		:	:	
Db	783	KVIKKEGKAAEAVAAVGTGATTAAVMAAAGIAAIGPAKELEAERSLMSSPEDLTkdFEE	842				
Qy	200	QPGNTVSSGQEDFPSV-LLETAASLPSLSPLSTVSFKEHGYLGNL SAVSSSEG TIEETLN	258				
		:	: :	:	:		
Db	843	LKAEVDVTkDIKPQLELIEDEEKLKETEPVEAYVIQKEREVTKGPAESPDEG-ITTTEG	901				
Qy	259	EASKELPERATNPFVNRLAEFSELEYSEMGS SFKGS PKGESAILVENTK-EEVIVRSKD	317				
			:	: : :	:	:	:
Db	902	EGECEQTPEELEPVEKQGVDDIEKFE--DEGAGFEES--SETGDYEEKAETEEAEPEED	957				
Qy	318	KEDLVC-SAALHSP-----QESPVGKEDRVVSPEKTMdIFNEMQMSV	358				
		: :		:		:	
Db	958	GEEHVCVSASKHSPTEDDEESAKAEADAYIREKRESVASGDDRA---EEDMD---EAIEKG	1011				
Qy	359	VAPVREEYADFKPFEQAWEVK-DTYEGSRDVLAAARANVESKVDRCLED SLEQ-----	410				
		:	: : :	: :	:	:	:
Db	1012	EAEQSEEEADEE--DKAEDAREEYEPEK--MEAEDYMAVVDKAAEAGGAEEQYGFLLT	1067				
Qy	411	--KSLGKDSEGR-----NEDASFPSTPEPVKDSSRAYITCASFTSATESTT	454				
			:	:	:	:	: : :
Db	1068	PTKQLGAQSPGREPASSIHDETLPGGSESEATASDEENREDQPEEFTATSGYTQSTIEIS	1127				
Qy	455	ANTFPL-----LEDHTSENKTDEK-----KIEERKAQIITEKTS-PKTSNPFVLAV	499				
		: :	: :	: :	:	: : :	
Db	1128	SEPTPMDEMSTPRDVMSDETNNETESPSQEFVNITKYESSLYSQEYSKPADVTPLNGFS	1187				
Qy	500	QDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDL---	556				
		: :	: :	:	:	:	: : :
Db	1188	EGSKTD--ATDGKDYNASASTISPPSSMEED---KFSRSALRDAYCSEVKASTTLdIKDS	1242				
Qy	557	--VQTSEAIQESLYPTAQLCP-----SFE-----EAEATPSPVLPDIV	592				
		: : :		:		: :	
Db	1243	ISAVSSEKVS PSKSPSLSPSPSPLEKTPLGERSVNFSLTPNEIKVSAEAEVAPVSPEVT	1302				
Qy	593	ME-----APLNSLLPSAG-----ASVVQ-----	610				
			: :		:		
Db	1303	QEVVEEHCASPEDKTLEVSPSQSVTGSAGHTPYQSPtDEKSSHLPTEVIEKPPAVPVS	1362				
Qy	611	-----PSVSPLEAPPPVSYDSIK--LEPENPPP-----YEEAMNVALKALG	649				
		:	:			: :	
Db	1363	FEFSDAKDENERASVSPMDEPVPDSESPIEKVLSPLRSPPLIGSESAYESFLSADDKASG	1422				
Qy	650	TKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPD-FSNYSEIA-----KF	701				
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Db 1423 -----RGAESPF-----EEKSGKQGSPDQVSPVSEMTSTSLYQDKQ 1458
 Qy 702 EKSVP EHAELVEDSSPE-----SEPVDLFSDDSIPEVPQTQ-----EEAV 741
 | : | : || | | : | : : | || | :
 Db 1459 EGKSTDFAPIKEDFGQEKKTDDVEAMSSQPALALDERKLGDVSPQTQIDVSQFGSFKEDTK 1518
 Qy 742 MLMKE-----SLTEVSETVAQ----HKEERLSASPQELG-----KPYLESFQPNLHSTK 786
 | : | | | | || : | | | : : | : | : ||
 Db 1519 MSISEGTVSDKSATPVDEGVAEDTYSHMEGVASVSTASVATSSSFPEPTTDDVSPSLH--- 1575
 Qy 787 DAASNDIPTLTk-KEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIEIDEF 845
 | | | : : : : | : : : || : :
 Db 1576 --AEVGSPHSTEVDDSLSVSVVQTPTT-FQETEMSPSKEECPR----- 1615
 Qy 846 PTFVSAKDDSPKLAKEYTDLE--VSDKSEIANIQSGADSLPCLELPCDLSFKN----- 896
 | : | | || | | : : | : : | : : | : | | : :
 Db 1616 PMSISPPDFSPKTAKSRTPVQDHRSEQSSM-SIEFGQES-PEQSLAMDFSRQSPDHPTVG 1673
 Qy 897 -----IYPKDE-VHVSDEFSENRRSSVSKASISPSNV 926
 | | : | : | | | : || : ||
 Db 1674 AGVLHITENGPTVDYSPSDMQDSSLSHKIPMEEPSYTDNDLSELISVSQVEASPSTS 1733
 Qy 927 SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAE 970
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 Db 1734 SAHTP-SQIASPLQEDTLSDVAPPR-----DMSLYASLTSE 1768

RESULT 10

US-09-149-476-411

; Sequence 411, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,163

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/047,600

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,615

; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312

; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,880
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060

; EARLIER FILING DATE: 1997-10-02

Query Match 4.9%; Score 286; DB 4; Length 92;
Best Local Similarity 56.0%; Pred. No. 2.2e-11;
Matches, 51; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

Qy 1064 NSALGHVNSTIKELRRFLVDDLVDSIKFAVLMWVFTYVGALFNGLTLLILALISLFSIP 1123
|:|: |:| :| : ||||:||||| || ||: ||||:||||:||||| : :||:|
Db 2 NAAMVHINRALKLIIRLFLVEDLVDSLKLAVFMWLMTYVGAVFNGITLLILAELLIFSVP 61
Qy 1124 VIYERHQVQIDHYLGLANKSVKDAMAKIQAK 1154
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Db 62 IVEKYKTQIDHYVGIARDQTKSIVEKIPSK 92

RESULT 11

US-08-973-462-8

; Sequence 8, Application US/08973462B

; Patent No. 6191270

; GENERAL INFORMATION:

; APPLICANT: DRUILHE, PIERRE

; APPLICANT: DAUBERSIES, PIERRE

; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES

; FILE REFERENCE: 0660-0125-0 PCT

; CURRENT APPLICATION NUMBER: US/08/973,462B

; CURRENT FILING DATE: 1998-02-06

; EARLIER APPLICATION NUMBER: PCT/FR96/00894

; EARLIER FILING DATE: 1996-06-12

; EARLIER APPLICATION NUMBER: FR 95/07007

; EARLIER FILING DATE: 1995-06-13

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 1786

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide

US-08-973-462-8

Query Match 4.8%; Score 279.5; DB 3; Length 1786;
Best Local Similarity 20.1%; Pred. No. 4.4e-09;
Matches 261; Conservative 220; Mismatches 518; Indels 297; Gaps 60;

Qy 33 EDEEEEEEEDEEDEDLEELVLERKPAAGLSAAAVPPAAAPLLDFSSDS-----VP 87
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Db 225 EKVEESVEENDEESVEENVEE-NVEENDDG---SVASSVEESIASSVDESIDSSIEENVA 280
Qy 88 P-----APRGPLPAAPPAAPERQPSWERSPA-----APAPSLPPAAAV-LPSKLPEDDE 135
| || || : : || | : | : : | : : | :| :|
Db 281 PTVEEIVAPSVVESVAPSVEESVEENVEESVAENVEESVAENVEESVAENVEESVAENVE 340
Qy 136 PPARP-----PPPPPAGASPLAEPAPPPSTPAAPKRRGSGSVDETFLFALPAASEPVIPS 189
| | :| : || : : || | : : :| | |
Db 341 EIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESVEENVEESVAENV--EESVAENVEES 398
Qy 190 SAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASL--PSLSPLSTVSFKEHGYLGNL SAVS 247

Db	399	VAENVEESVAE--NVEESVAENVEEIVAPTVEEIVAPTVEEIVAPSVVE-----SVAP	449
Qy	248	SSEG TIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGS SFGSPKGESAILVENT	307
Db	450	SVEESVEENVEESVAENVEESVAENVEESVAENVE-----ES--VAENV	491
Qy	308	KEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVPVREEYA	367
Db	492	EESV---AENVEESVA----ENVEESVAENVEEIVAP--TVE-----EIVAPTVEEIV	535
Qy	368	DFKPF EQ-AWEVKD TYEGSRDVL AARANVESKVDRCLEDSLEQKSLGKDSEGRN-EDAS	425
Db	536	APSVVESVAPSVEESVEENVEESVAE-NVEESVAEN-VEESVAENV--EESVAENVEEIV	591
Qy	426	FPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKAQIITE	485
Db	592	APTVEEIVAPTVEEIVA----PSVVESVA----PSVEESVEEN-----VEESVAENVEE	637
Qy	486	KTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATG	545
Db	638	SVAENVEESVAENVEEIVAPTVEEIVAPTVEEIVAPSVVESVAPS-VEESVEENVEESVA	696
Qy	546	TKIAYETKVDLVQTS--EAIQESLYPTAQ--LCPSFEEAEATPSPVLPDIVMEAPLNSLL	601
Db	697	ENVE-ESVAENVEESVAENVEESVAENVEEIVAPTVEEIVA---PTVEEIVAPSVVESVA	752
Qy	602	PSAGASV-----VQPSVSPLEAPPPVSYDSIKLE	630
Db	753	PSVEESVEENVEESVAENVEESVAENVEESVAENVEESVAPTVEEIVAP-----SVE	804
Qy	631	PENPPPYEEAM-----NVALKALGTKEGIKEPESFNAAVQETEAPYISIACDLIK	680
Db	805	ESVAPSVEESVAENVATNLSNDNLLS NLLGGIETEEIKDSILNEIEEVKENVTTILENVE	864
Qy	681	ETKLSTEPSPDFSNYSEIAK-----FEKS VPEHAELV-----EDSSPESEPVDLF--	725
Db	865	ET--TAESVTTFSNILEEQENTITNDTIEEKLEELHENVLSAALENTQSEEKKEVIDV	922
Qy	726	-----SDDSIPEVPQTQEEAVMLMKESLTE-----VSETV	755
Db	923	IEEVKEEVATTLIETVEQAEKSANTITEIFENLEENAVESNENVAENLEKLNETVFNTV	982
Qy	756	AQHKEERLSASPQELGKPYLES--FQPNLHSTKDAASNDIPTLTk--KEKISLQMEE---	808
Db	983	LDKVEETVEISGESLENNEMDKAFFSEIFDNVKG IQENLLTGMFRSIETSIVIQSEEKVD	1042
Qy	809	FNTAIYSN--DLLSSKEDKIKESETFSDSSPI-EIIDEF-----PTFVS	850
Db	1043	LNENVVSSILDNIENMKEGLLNKLENISSTEGVQETVTEHVEQNVYVDVDVPAMKDQFLG	1102
Qy	851	AKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPKDEVHVSDEFS	910
Db	1103	ILNEAGGLKEMFFNLEDVFKSE-----SDVITVEEIKDEPVQKEV-EKETVSIIEEME	1154
Qy	911	ENRSSV---SKASISPSNVSALEPQTEMGSIVKSKSIT-KEAEKKLPDTEK-----EDR	961

Db 1155 ENIVDVLEEEKEDLTDKMIDAVEESIEISSDSKEETESIKDKEKDVSLVVEEVQDNDMDE 1214

Qy 962 SLSAVL-----SAELSKTSV-VDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIA 1015
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Db 1215 SVEKVLELKNMEEELMKDAVEINDITSKLIETQELNEVEADLIKDME-----K 1263

Qy 1016 LALLSVTISFRIYKGVIIQA----IQK-SDEGHPFRAYLESEVA---ISEELVQKYSN--S 1065
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Db 1264 LKELEKALS-EDSKEIIDAKDDTLEKVIEEEHDITTTLDEVVELKDVEEDKIEKVSDLKD 1322

Qy 1066 ALGHVNSTIKELRRLEFLVDDLVDLSLKFAVLMMWFTYVGALFNGLTLLILALISLFSIPVI 1125
 : :||:: | :::: | : ::

Db 1323 LEEDILKEVKEIKE--LESEILEDYK-----ELKTIETDIL 1356

Qy 1126 YERHQVQIDHYLGLANKS--VKDAMAKIQAKIPGLK 1159
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Db 1357 EEKKEIEKDHFEKFEKEAEIKDLEADILKEVSSLE 1392

RESULT 12

US-08-769-309A-5

; Sequence 5, Application US/08769309A

; Patent No. 5741890

; GENERAL INFORMATION:

; APPLICANT: Scott, John D.,

; APPLICANT: Nauert, Brian J.,

; APPLICANT: Klauck, Theresa M.

; TITLE OF INVENTION: Protein Binding Domains of Gravin

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower/233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/769,309A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5741890and, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27866/33451

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

; TELEFAX: 312-474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1780 amino acids

; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-769-309A-5

Query Match 4.5%; Score 265.5; DB 1; Length 1780;
Best Local Similarity 20.8%; Pred. No. 3.4e-08;
Matches 264; Conservative 146; Mismatches 486; Indels 371; Gaps 51;

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Qy      11 SSSTDSPRRPPPA-----FKYQFVTE-----PEDE----EDEEEEEDEEED 47
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Db      277 SKSAESPTSPVTSETGSTFK-KFFTQGWAGWRKKTSTRKPKEDVEASEKKKEQEPEKVD 335

Qy      48 DEDLEEELEVLERKPAAGLSAAVPPAAAA--PLLDFSSDSVPPAPRGPLPAAPPAAPERQ 105
      | : : | | | | | | | | : | | : | | : | |
Db      336 TEEDGKAEVASEKLTASEQAHQPQEPASAEHPRLSAEYEV-----ELPS-----EEQ 383

Qy      106 PSWERSPAAPAPSLPPAAVLPSKLP-----EDDEPPARPPPPPPAGASP 150
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Db      384 VSGSQGPSEKPA-PLATEVFDEKIEVHQEEVVAEVHVSTVEERTEEQKTEVEETAGSVP 442

Qy      151 L-----AEP--AAPPSTPAAPKRRGSGSVDETFLFALPAASEPVIPISSAEKIMDLMEQP 201
      || | | | | | | | | : | | : | : : |
Db      443 AEELVGMDAEPQEAEPAKELVKLKETCVSGEDPTQGADLSPDEKVLSPKPEGVVSEVEML 502

Qy      202 GNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLG-----NLSAVSSSEGTI 253
      : : | | | : | | | : | | | : : | :
Db      503 SSQERMKVQGSPLKKLFTSTGLKKLS-----GKKQKGRGGGDEESGEHTQVPADSPDSQ 557

Qy      254 EETLNEASKELPERATN-PFVNRDLAEFSELEYSEMGSSEFKGSPKGESAILVENTKEEVI 312
      || | : | | | : : || | : : | | : | : |
Db      558 EEQKGESSASSPEEPEEITCLEKGLAEVQQDGEAEEGATSDGEKKREGVTPWASFKKMVT 617

Qy      313 VRSK-----DKE---DLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVAPV 362
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Db      618 PKKRVRRPSESDKEDELKVKSATLSSTEST-----ASEMQEEMKGSVEEPK 664

Qy      363 REEYADFKPFQAWEV-----KDTYEGS 385
      || : | | | | | | | | | |
Db      665 PEEPKRKVDTSVSWEALICVGSSKKRARRRRSSSDEEGGPKAMGGDHQKADEAGKDKETGT 724

Qy      386 RDVLA-----ARANVESK-----VDRKCLEDLSLEQKSLGKDS 417
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Db      725 DGILAGSQEHDPGQGSSEPEQAGSPTEGEGVSTWESFKRLVTPRKKSLSKLEKS--EDS 782

Qy      418 -EGRNEDASFPSTPEPVKDSS-----RAYITCASFTSATE--ST 453
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Db      783 IAGSGVEHSTPDT-EPGKEESWVSIKKFIPGRRKKRPDQKQEQAPVEDAGPTGANEDDSD 841

Qy      454 TANTFPILLEDHTSENKTDE-----KKIEERKAQIITEKTSPKTSNPFLVAVQD---- 501
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Db      842 VPAVPLSEYDAVEREKMEAQQAQKGAEQPEQKAATEVSKELSESQVHMAAAVADGTRA 901

Qy      502 -----SEADYVTTDTLSK-----VTEAAVSNMPEG- 526
      : || : | : | : | | : | |
Db      902 ATIIERSPSWISASVTEPLEQVEAEAAALLTEEVLEREVIAEEEPPTVTEP----LPENR 957

Qy      527 -----LTPDLVQEA-CESELNEATGTKI-AYETKVDLVQTSEAIQESLYPTAQ 572
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Db      958 EARGDTVSEAEALTPEAVTAAETAGPLGSEEGTEASAAEETTEMVSAVSQLTDSPTDTEE 1017
Qy      573 L-----CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVS 623
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Db      1018 ATPVQEVEGGVPDIEEQERRTQEVQLQAVAEKVKEESQLPGTG-----GPEDVLQPVO 1069
Qy      624 YDSIKLEPENPPPYEEA-----MNVALK-----ALGTKEGIKEPESFNAAVQE 666
      : | | | || : || | | ||| | |
Db      1070 ----RAEAERPEEQAEASGLKKETDVVLKVDAQEAKTEPFTQGKVVGQTTPESEFEKAPQV 1125
Qy      667 TEAPYISIIACDLIKETKLSTEPSD--FSNYSEIAKFEKSVPEHAELVEDSSPES--EPV 722
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Db      1126 TES-----IESSELVTTCQAETLAGVKSQEMVMEQAIP-----PDSVETPT 1166
Qy      723 DLFSDDSIPI-----EVPQTQEEAVMLMKESLTVSETVAQH----KEERLSASPQELGKPY 774
      | : | | : | | : | : | : | : | | : :|
Db      1167 DSETDGSTPVADFDAPGTTQ-----KDEIVEIHEENEVHLVPVRGTEAEAVPAQKERPP 1220
Qy      775 LESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFS 834
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Db      1221 APSSFVFQEETKE-----QSKMEDTLEHTDKEVSVETVSILSKTEGTQEADQYA 1269
Qy      835 DSSPIEI-----IDEFPTFVS AKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPC 885
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Db      1270 DEKTKDVPFFEGLEGSIDTGITVSREKVTEVALKGEGETEEAECKKDDALELQSHAKSPPS 1329
Qy      886 LELPCDLSF-----KNIYPKDEVHVSDEFSENRSS-----VSKASISPSNVSALEPQTE 934
      | : : : ||:| | : : ||| : || : : |
Db      1330 ---PVEREMVVQVEREKTEAEPHVNEEKLEHETAVTVSEEVSKQLLQTVNVPIIDGAKE 1386
Qy      935 MGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVF-- 992
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Db      1387 VSSLEGSPPPCLGQEEAVCTKIQVQSSEASFTLTAAAEKVK--LGETANILETGETLEP 1444
Qy      993 -GASLFL 998
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Db      1445 AGAHLVL 1451

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RESULT 13

US-08-994-570-5

; Sequence 5, Application US/08994570

; Patent No. 6090929

; GENERAL INFORMATION:

; APPLICANT: Scott, John D.,

; APPLICANT: Nauert, Brian J.,

; APPLICANT: Klauck, Theresa M.

; TITLE OF INVENTION: Protein Binding Domains of Gravin

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower/233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,570
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090929and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33451
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-994-570-5

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Query Match          4.5%; Score 265.5; DB 3; Length 1780;
Best Local Similarity 20.8%; Pred. No. 3.4e-08;
Matches 264; Conservative 146; Mismatches 486; Indels 371; Gaps 51;

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Qy      11 SSSTDSPRRPPPA-----FKYQFVTE-----PEDE----EDEEEEEDEEED 47
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Db      277 SKSAESPTSPVTSETGSTFK-KFFTQGWAGWRKKT SFRKPKEDVEVEASEKKKEQEPEKVD 335

Qy      48 DEDLEELEVLERKPAAGLSAAAVPPAAAA--PLLDFFSSDSVPPAPRGPLPAAPPAAPERQ 105
      | : : | | | | | | | | | : | | | | |
Db      336 TEEDGKAEVASEKLTASEQAHPQEPAESAHEPRLSAEYEKV-----ELPS-----EEQ 383

Qy      106 PSWERSPAAPAPSLPPAAVLPSKLP-----EDDEPPARPPPPPPAGASP 150
      | : | : | : | | | | | : | : | | |
Db      384 VSGSQGPSEKPA-PLATEVFDEKIEVHQEEVVAEVHVSTVEERTEEQKTEVEETAGSVP 442

Qy      151 L-----AEP--AAPPSTPAAPKRRGSGSVDET L FALPAASEPVI PSSAEKIMDLMEQP 201
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Db      443 AEELVGMDAEPQEAEPAKELVKLKETCVSGEDPTQGADLSPDEKVL SKPPEGVVSEVEML 502

Qy      202 GNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLG-----NLSAVSSSEGTI 253
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Db      503 SSQERMKVQGSPLKKLFTSTGLKKLS-----GKKQKGKRGGGDEESGEHTQVPADSPDSQ 557

Qy      254 EETLNEASKELPERATN-PFVNRDLAEFSELEYSEMGS SFGSPKGESAILVENTKEEVI 312
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Db      558 EEQKGESSASSPEEPEEITCLEKGLAEVQQDGEAE EGATSDGEKKREGVTPWASFKKMVT 617

Qy      313 VRSK-----DKE---DLVCSAALHSPQESPVGKEDRVVSPEKTM DIFNEMQMSVVAPV 362
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Db      618 PKKRVRRPSESDKEDEL DKVKSATLSSTEST-----ASEMQEEMKGSVEEPK 664

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Qy 363 REEYADFKPFEQAWEV-----KDTYEGS 385
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 Db 665 PEEPKRKVDTSVSWEALICVGSSKKRARRRRSSSDEEGGPKAMGGDHQKADEAGKDKETGT 724
 Qy 386 RDVLA-----ARANVESK-----VDRKCLEDSELEQKSLGKDS 417
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 Db 725 DGILAGSQEHDPGQGSSSPEQAGSPTEGEGVSTWESFKRLVTPRKKSLSKLEKS--EDS 782
 Qy 418 -EGRNEDASFPSTPEPVKDSS-----RAYITCASFTSATE--ST 453
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 Db 783 IAGSGVEHSTPDT-EPGKEESWVSIKKFIPGRRKKRPDQKQEQAPVEDAGPTGANEDDSD 841
 Qy 454 TANTFPLLEDHTSENKTDE-----KKIEERKAQIITEKTSPKTSNPFLVAVQD---- 501
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 Db 842 VPAVVLSEYDAVEREKMEAQQAQKGAEQPEQKAATEVSKELSESQVHMAAAVADGTRA 901
 Qy 502 -----SEADYVTTDTLSK-----VTEAAVSNMPEG- 526
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 Db 902 ATIIEERSPSWISASVTEPLEQVEAEAALLTEEVLEREVIAEEEPPTVTEP-----LPENR 957
 Qy 527 -----LTPDLVQEA-CESELNEATGTKI-AYETKVDLVQTSEAIQESLYPTAQ 572
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 Db 958 EARGDTVVSEAELTPEAVTAAETAGPLGSEEGTEASAAEETTEMVSAVSQLTDSPDTTEE 1017
 Qy 573 L-----CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVS 623
 | || | || : : | || | | : ||
 Db 1018 ATPVQVEVEGGVPDIEEQERRTQEVLLQAVAQKVKESQLPGTG-----GPEDVLQPVQ 1069
 Qy 624 YDSIKLEPENPPPYEEA-----MNVALK-----ALGTKEGIKEPESFNAAVQE 666
 : | | | || : | || | | | || | |
 Db 1070 ----RAEAERPEEQAEASGLKKETDVVLKVDAQEAKEPFTQGKVVGQTTPESEFEKAPQV 1125
 Qy 667 TEAPYISIACDLIKETKLSTEPSPD--FSNYSEIAKFEKSVPEHAELVEDSSPES--EPV 722
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 Db 1126 TES-----IESSELVTTCQAETLAGVKSQEMVMEQAIP-----PDSVETPT 1166
 Qy 723 DLFSDDSIP----EVPQTQEEAVMLMKESLTEVSETVAQH----KEERLSASPQELGKPY 774
 | :| | | : | | : | : | : | | : | :|
 Db 1167 DSETDGSTPVADFDAPGTTQ-----KDEIVEIHEENEVHLVPVRGTEAEAVPAQKERPP 1220
 Qy 775 LESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFS 834
 | ||: | : :| : : : | | : :| : :
 Db 1221 APSSFVFQEETKE-----QSKMEDTLEHTDKEVSVETVSILSKTEGTQEQADQYA 1269
 Qy 835 DSSPIEI-----IDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPC 885
 | : : || | | | | : | : :| | | |
 Db 1270 DEKTKDVPFFEGLEGSIDTGITVSREKVTEVALKGEGTEEAECKKDDALELQSHAKSPPS 1329
 Qy 886 LELPCDLSF-----KNIYPKDEVHVSDEFSENRSS-----VSKASISPSNVSALEPQTE 934
 | : : : ||:| | : : ||| : | : : |
 Db 1330 ---PVEREMVVQVEREKTEAEPHTVNEEKLEHETAVTVSEEVSKQLLQTVNVPIIDGAKE 1386
 Qy 935 MGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVF-- 992
 : | : | : : : : | | : | | : | :|
 Db 1387 VSSLEGSPPPCLGQEEAVCTKIQVQSSEASFTLTAAAEKEKV--LGETANILETGETLEP 1444
 Qy 993 -GASLFL 998

Db 1445 AGAHLVL 1451

RESULT 14

```

; Sequence 4463, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;   APPLICANT: Lynn Doucette-Stamm et al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS
;   TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: GTC-007
;   CURRENT APPLICATION NUMBER: US/09/134,001C
;   CURRENT FILING DATE: 1998-08-13
;   PRIOR APPLICATION NUMBER: US 60/064,964
;   PRIOR FILING DATE: 1997-11-08
;   PRIOR APPLICATION NUMBER: US 60/055,779
;   PRIOR FILING DATE: 1997-08-14
;   NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4463
;   LENGTH: 2137
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4463

```

Qy	159	STPAAPKRRGSGSVDETFLFALPAASEEPVSSAEKIMDLMEQPGNTVSSGQEDFPSVLL	218
Db	990	STSTSTSDSASTSTSE-----SESDSASTSLSESTSTSVSDSTSTSTSDSASMSASESE	1043
Qy	219	TAASLPSLSPLSTVSVFKEHGYLGNL SAV---SSSEGTIEETLNEASKELPERATNPFVNR	275
Db	1044	SNSKSTSLSESTSTSL S-----GTSASTSDSASTSTSESESDSTSTSLSESTSTSLSGS	1098
Qy	276	DLAEFSELEYSEMGSFFKGS PKGESAILVE-----NTKEEVIVRSKDKEDLVC	323
Db	1099	TSASTSD---SASTSTSESDSTSESLSESLSTSVSDSTSASTSESESDSTSESESN	1155
Qy	324	SAALHSPQESPVGKEDRVVSPEKTM DIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYE	383
Db	1156	STSLSGSLSTSI SDSTSTSTSDSASTSTSESESDSTSTSLSE-----STSTSLSDSTS	1208
Qy	384	GSRDVLAAARANVESKVDRKCLED SLEQK---SLGKDSEGRNEDASFPSTPEPVKDSSRAY	440
Db	1209	TSTSESASTSTSES--DSTSESTSLSESTSTSVSDSTSASTSDSASTSTSVSDSESA	1266
Qy	441	ITCASFTSATESTTANTFPLEDHTSE--NKTDEKKIEERKAQIITEKTS PKTSNPFLVA	498
Db	1267	ISESLSTSVSDSTSTSTSDSASTSTSESDSTSESTSLSESI STSVSDSTSASTSDSASTS	1326
Qy	499	VQDSEADYVTTD-----TLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYE	551

Db 1327 TSESESDSASTSLSGSTSTSLSDSTSTSTSDSASTSTSESDSERASTSLSGSTSTSLSDS 1386

Qy 552 TKV---DLVQTSEAIQESLYPTAQLCPSPFEEAEATPSPVLPDIVMEAPINSLLPSAGASV 608
| | | | : : | | : | | : : | | |

Db 1387 TSTSTSDSASTSTSVSDS-----NSASTSLSGSLSTSVSDSTSTSTSDSASAST 1435

Qy 609 VQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALK-ALGTKEGIKEPESFNAAVQET 667
| | | | : : : : : | : | : : | :

Db 1436 ---SESDSERA-----STSLSGSTSTSTSDSTSTSTSDSASTSTSVSESNSTSTSTSES 1486

Qy 668 EAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESEPVDFLSD 727
: : | | | | : : : : : | | | : : | :

Db 1487 LSTSVS-----DSTSTSTSDSASTSTSVSDSDSASTSSSESV--STSDSESTSTSTST 1536

Qy 728 DSI---PEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQE-----LGKPYLESFQ 779
| | | : : : | : | | : : : : | | | |

Db 1537 DSASTSTSVSESNSTSTSLSGSTSTSVSDSTSTSTSDSASASTSESDSDSASTSSSESVS 1596

Qy 780 PNLH-----STKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFS 834
: : | | : : | : : : : | : : : : | | : |

Db 1597 TSVSDSTASTSESASTSTSVSDSNSASTSLSESTSTSLSDSTSMSTSDSASTSTSESDS 1656

Qy 835 DSSPIEIID-----EFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADS 882
| | : : | | | | : : : : : | | : : : | | :

Db 1657 DSASTSLSDSTSTSVSESTSTSTSTSVSASNSTSTSLSDSRSTSLSDSTSTSTSESGSTS 1716

Qy 883 LPCLELPCDLSFKNIYPKDEVHVSDEFSEN--SSVSKASISPSNVSALEPQTEMGSIVK 940
| | : : : | | | : : | : : | : | : : : |

Db 1717 TS--ESDSDSASTSLSESTSTSTSDSTSTSTSDSASTSMSVSDSNRASTSLSDSTSTSVS 1774

Qy 941 SKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVD 978
: : | | | | | | : | | |

Db 1775 DSTSASTSESASTSTRESESTASTSLSESTSTSVSD 1811

RESULT 15

US-09-621-976-4600

; Sequence 4600, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 4600

; LENGTH: 75

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: 58

; OTHER INFORMATION: Xaa = His,Pro


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; NAME/KEY: UNSURE
; LOCATION: 28
; OTHER INFORMATION: Xaa = Met,Val
; NAME/KEY: UNSURE
; LOCATION: 19
; OTHER INFORMATION: Xaa = Pro,Gln
; NAME/KEY: UNSURE
; LOCATION: 53
; OTHER INFORMATION: Xaa = Ser,Tyr
US-09-621-976-4600

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Query Match          4.4%; Score 256.5; DB 4; Length 75;
Best Local Similarity 67.0%; Pred. No. 1.2e-09;
Matches 59; Conservative 3; Mismatches 11; Indels 15; Gaps 3;

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Qy      1 MEDIDQSSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEELEVLERK 60
        |||:||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MEDLDQSPLVSSS-DSPPRXQPAFKYQFXREPEDEE-----EDLEEELEVLERK 47

Qy      61 PAAGLSAAAV--PPAAAPLLDFSSDSV 86
        ||||| || | ||| |||:||| :| |
Db      48 PAAGLXAAPVXTAPAAGAPLMDFGNDFV 75

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Search completed: September 3, 2004, 16:10:34
Job time : 28.9601 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2004, 16:00:14 ; Search time 24.8344 Seconds
(without alignments)
4504.667 Million cell updates/sec

Title: US-09-830-972-2
Perfect score: 5848
Sequence: 1 MEDIDQSSLVSSSTDSPRP.....VKDAMAKIQAKIPGLKRKAD 1163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	789.5	13.5 776	2	A46583	neuroendocrine-spe
2	685	11.7 208	2	I60904	neuroendocrine-spe
3	671	11.5 267	2	A60021	tropomyosin-relate
4	517	8.8 2484	2	T26216	hypothetical prote
5	503.5	8.6 2607	2	T26215	hypothetical prote
6	328.5	5.6 5327	2	T13564	microtubule-associ
7	322	5.5 7962	2	I38346	elastic titin - hu
8	320	5.5 222	2	T26213	hypothetical prote
9	304.5	5.2 873	2	A47283	calphotin - fruit
10	302.5	5.2 1829	2	T24583	hypothetical prote
11	295.5	5.1 865	2	A47282	calcium-binding pr
12	292	5.0 3507	2	T34513	hypothetical prote
13	291.5	5.0 2364	2	A56577	microtubule-associ

14	288.5	4.9	971	2	T19431	hypothetical prote
15	284	4.9	2464	1	QRMSF1	microtubule-associ
16	281	4.8	3488	2	T34418	hypothetical prote
17	279.5	4.8	1262	2	T22523	hypothetical prote
18	277	4.7	1621	2	A82255	hypothetical prote
19	275.5	4.7	3924	2	S37431	ankyrin 2, neurona
20	275	4.7	1299	2	T47182	hypothetical prote
21	273.5	4.7	1029	2	T30351	mucin-like protein
22	273.5	4.7	1274	2	T16251	hypothetical prote
23	273	4.7	1558	2	B71603	RESA-H3 antigen PF
24	272.5	4.7	3534	2	T42567	tegument protein 2
25	270	4.6	1230	2	T22458	hypothetical prote
26	269.5	4.6	2187	2	T30826	nascent polypeptid
27	267	4.6	1684	2	JW0057	gravin - human
28	265.5	4.5	1828	2	A40115	microtubule-associ
29	263	4.5	1825	2	S13507	microtubule-associ
30	261.5	4.5	1087	1	QFMSH	neurofilament trip
31	261	4.5	606	2	A43427	neurofilament trip
32	261	4.5	2570	2	T17451	fimbriae-associate
33	260	4.4	1804	2	T34518	nestin - golden ha
34	259.5	4.4	1020	1	QFHUH	neurofilament trip
35	259	4.4	1510	2	T33100	hypothetical prote
36	258.5	4.4	1830	2	A37981	microtubule-associ
37	257	4.4	1224	2	T14007	microtubule-associ
38	256	4.4	2361	2	T25752	hypothetical prote
39	254.5	4.4	6642	2	T29757	protein UNC-89 - C
40	254	4.3	1616	2	G64242	cytadherence-acces
41	254	4.3	3381	2	T42389	versican precursor
42	253	4.3	3421	1	WZBEB6	367K tegument prot
43	252.5	4.3	5170	2	T15348	hypothetical prote
44	251	4.3	1824	1	QRHUMT	microtubule-associ
45	250.5	4.3	4377	2	A55575	ankyrin 3, long sp

ALIGNMENTS

RESULT 1

A46583

neuroendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: A46583; I60903

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 421-776 <ROE2>
A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309
C;Genetics:
A;Gene: GDB:RTN1; NSP
A;Cross-references: GDB:203968; OMIM:600865
A;Map position: 14q21-14q22

Query Match 13.5%; Score 789.5; DB 2; Length 776;
Best Local Similarity 31.2%; Pred. No. 3.5e-25;
Matches 243; Conservative 115; Mismatches 252; Indels 169; Gaps 28;

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Qy      487 TSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGT 546
      : | : | ||: : : | : | || : | : :
Db      65 SGPARGSP--VAMETASTGVAGVSSAMDHTFSTTSKDGE-----SCYTSLI-----S 110

Qy      547 KIAYETKVDLVQTSEAIQ-ESLYPTAQLCPSFEEAEATPSPVLPDI--VMEAPLNS----- 599
      | | : | : : | : : | | | ||| : : | |
Db     111 DICYPQEDSTYFTGILQKENGHVITISESP---EELGTPGPSLPDVPGLIESRGLFSSDSG 167

Qy      600 --LLPSAGASVVQPSVSPLEAPPPVSY-----DSIKLEPENPPPYEEA-----M 641
      : | : | : ||: : | : : : : | | :
Db     168 IEMTPAESTEVNKILADPLDQMKAEAYKYIDITRPEEVKHQEQHHPELEDKDLDFKNKDT 227

Qy      642 NVALKALGTKEGIKEPE-----SFNAAVQETEAPYISIACDLIKETKLSTE-PSP 690
      : : : | ||: ||: : : : : | ||| || : | : : : : |
Db     228 DISIK----PEGVREPDKPAPVEGKIIKDHLLEESTFAPYID---DLSEEQRRAPOITTP 280

Qy      691 DFSNYSEIAKFEKSVPEHAELVEDSSPESEPVDF--SDDSIPEV----PQTQEEAVMLMK 745
      : || | : : || : : | | | : | | : :
Db     281 VKITLTEIE-----PSVETTTQEKTPKQDICKPSPDTVPTVTVSEPEDDSPGSITPP 334

Qy      746 ESLTEVSETVAQHK-----EERLSASPQELGKPYLESFQP----NLHSTKDAASND----- 792
      | || | : | | : : | : | | : | : :
Db     335 SSGTEPSAAESQKGKSISEDELITAIKEAKGLSYETAENPRPVGQLADRPEVKARSGPPT 394

Qy      793 IPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKI----- 827
      ||: | | : : : | | : : || :
Db     395 IPSPLDHEASSAESGDSEIELVSEDPM--AAEDALPSGYVSFGHVGGPPPPSPASPSIQYS 452

Qy      828 ---KESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEI-----ANIQSG 879
      : | | || | : | | || : ||| : : : | | :
Db     453 ILREERAEELDS---ELIIESCDASSASEESPKREQDSPPMKPSALDAIREETGVRAEER 509

Qy      880 ADSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSI 939
      | | | | || : || | | | | ||| : | |
Db     510 APSRRGLAEPG--SFLD-YPSTEPQGPPEL-----PPGDGALEPETPM----- 549

Qy      940 KSKSLTKEAEKKLPDTEKEDRSLSAVLSAE-----LSKTSVVDLLLYWRD 984
      || ||: | : : : : | : | : |||||
Db     550 -----LPRKPEEDSSSNQSPAATKGPGPLGPGAPPPLLFLNKQKAIDLLYWRD 597

Qy      985 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGH 1044
      ||: ||: ||: | || ||| ||: ||| ||: ||| || ||||| ||: ||: ||: |||||
Db     598 IKQTGIVFGSFLLLLSLTQFSVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGH 657

```


Qy	28	FVTEPEDEE---DEEEEEDEEED-----DEDLEELEVL-----	57
		: : : :	
Db	1437	FGTESSEESQKADGNQENQEEEDVVAELNFHPIRQWRDEDVISLQSLKSLVAEVCITDV	1496
Qy	58	-----ERKPAAGLSAAAVPPAAAPL-LDFSSDSVPPAPRGPLPAAPPAAP--ERQPSW	108
		: : : : : :	
Db	1497	DASDVNEQDEESTLKILKVVPPSEPSLLELDFTND--PKVIHVPIPLMEPATMYLEEMVEW	1554
Qy	109	-----ERSPAAPAPSLPPAAAVLPS-----KLP-EDDEPPARPPPPPPA	146
		: : : :	
Db	1555	IIADAVKEVSEMEVVTSEISEMAPQVSESTCPIPEPLADLKLPVEDDEKTPEPEPVPG	1614
Qy	147	GASPLAEPAPPSTPAAPKRRGSGSVDETFLFALPAASEPVIPS-SAEKIMDLMEQPGNTV	205
		: : : :	
Db	1615	QVQERIPIEVEQAPTIPQRPPRAPKSE----LPKVAKPLDDSKSRVRFAPLNKLGRTY	1670
Qy	206	SSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNL SAVSSSEGTIEETLNEASKELP	265
		: : : : : :	
Db	1671	SEEQQK-----ELVESLE--RPLTIIT-----QQKPP	1695
Qy	266	ERAT-----NPFVNRDLAEFSELEYSEMGSSFKGSPKGESAILVENTKEEVIVRSKDKE	319
		: : : :	
Db	1696	EKPTEDIGALSPLSPNTLAEEYEEVPMMDMQS-----	1726
Qy	320	DLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQ-MSVVAPVREEYADFKPFQAWEV	378
		: : : :	
Db	1727	-----VPHSPQE----KQEEI--EALSEIIEEPQAMKEVE-----KPVESAPE-	1763
Qy	379	KDTYEGSRDVLAAARANVESKVDRKCLEDSL--EQKSLGKDSEGRNEDASFPSTPEPVKDS	436
		: : : : : :	
Db	1764	KD-----NESLEAPEIINEPIRRVLVETKIMGPGKSLNED----NDD-----	1801
Qy	437	SRAYITCASFTSATESTTANTFPLEDHTSENKTDEKKIEERKAQIITEKTSPKTSNPFL	496
		: : :	
Db	1802	-----DDDGSECLDSIGDLSE-----TIQRFN	1824
Qy	497	VAVQDSEADYVTTDTLSKVT-----EAAVSNMPEGLTPDLVQEACESELNEATGTKI	548
		: : : : : : :	
Db	1825	TSIDDPS---IRRDSFSSISSFGDRQKFRTAIENIRQDLLP-----	1862
Qy	549	AYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASV	608
		: : : : : : : : : : :	
Db	1863	-FQSSV-----SQYLRSSPNPSQQL-----LVTNLSMDSP-SDLSPNA----	1898
Qy	609	VQPSVSPLEAPPPVSYDSI-----KLEPENPPPYEEAMNVALKALGTKEGIKESFNAA	663
		: : : : : : : :	
Db	1899	-----PPVGFENTAQFLEKLQQEDRPSAEGSID-----SSGFQVD--HEG	1937
Qy	664	VQETEAPYISIACDLIKETKLSTEPSPDF-----SNYSEIAKFEKSVP	707
		: : : : : : : : :	
Db	1938	LDEFAAPPVH---DPMQKSVFGSLGSDDMKPGSQDDGFVFIERNEANEATLKKNQKMSSH	1994
Qy	708	HAELVEDS-----SPSEPVDFLSDDSIPEVPQTQEEAV-----MLMKESLTE	750
		: : : : : : : : : : :	
Db	1995	HNDVIEKNYFNDNAPTAALESPIAEAEARKLVQDAVESASEYKKQAVDSGDEIGRELLDN	2054

Qy 751 VSETVAQHKE-----ERLSASPQELGKPYLESFQP 780
 | : : | | | | : : : | : : |
 Db 2055 VEQKIEQVKEPIVDSLHKAYDGVGDFVHETVPNAVDDFVREAEKQLPESPVPEKIETPEP 2114

Qy 781 --NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDK-----IKES 830
 : : | | : : : : | : : | : : : :
 Db 2115 LVDIHDTVDKVHDEVNFLRREP-----TPPFETDDVAPLSDDKPQFGNQTPPEDE 2165

Qy 831 ETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGA----DSLPLCL 886
 | | : : | : : : : : | : : : : | : :
 Db 2166 TTFDRKGPLTIPEEVEKAAAQNNND---LDDFDPLVTSNTGAAFGAAVGAAGAAAVESLTEE 2222

Qy 887 ELPCDLSFKNI-----YPKDEVHVSDEFSENRRSSVSKASISPSNVSA-----LEPQTEM 935
 | : : : | | : : | : | : : | : :
 Db 2223 EMFGHQKFETVPRPPTPPKD---ISDE-----DVKPSTVNLGPSHHHSHPSPPH 2268

Qy 936 GSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGAS 995
 | : | : : : | : : : : | : : : : | : :
 Db 2269 HSILKHHG-----DAWIDFKTVPPCVLDVIYWRDAKKSIVLSLA 2308

Qy 996 LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAIS 1055
 | : | : : : | | | | : : | : : | : : | : : :
 Db 2309 LLVLFVLAKYPLLTVVVTSLLLALGAAAGFRVFKKVEAQIKKTDSEHPFSEILAQDLTLP 2368

Qy 1056 EELVQKYSNSALGHVNSTIKELRRLFLVDDLVDSLKFVILMWVFTYVGALENGLTLLILA 1115
 : | : : : | : : : | : : : | : : : | : : : | : :
 Db 2369 QEKVHAQADVFEHATCIANKLKKLVFVESPLESIKGLVLWSLTYYIASWFSGFTLAILG 2428

Qy 1116 LISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLK 1159
 | : : | : | : | : | : : : | : : : | : :
 Db 2429 LLGVFSVPKVYESNQEAIDPHLATISGHLKNVQNIIDEKLPFLR 2472

RESULT 5

T26215

hypothetical protein W06A7.3a - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T26215

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26215

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2607 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3a

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2;
 2586/2

Query Match 8.6%; Score 503.5; DB 2; Length 2607;
 Best Local Similarity 20.8%; Pred. No. 1e-12;
 Matches 280; Conservative 181; Mismatches 481; Indels 407; Gaps 52;

Qy 28 FVTEPEDEE---DEEEEEDEEED-----DEDLEEEVL----- 57
 | | | : | | : | | | | | | : | : |
 Db 1437 FGTESSEESQKADGNQENQEEEDVVAELNFHPIRQWRDEDVISLQSLKSLVAEVCITDV 1496
 Qy 58 -----ERKPAAGLSAAAVPPAAAAPL-LDFSSDSVPPAPRGPLPAAPPAAP--ERQPSW 108
 | : : | | : : | | | : | | : | | | |
 Db 1497 DASDVNEQDEESTLKILKVVPSEPSLLELDFDFTND--PKVIHVPIPIMEPATMYLEEMVEW 1554
 Qy 109 -----ERSPAAPAPSLPPAAAVLPS-----KLP-EDDEPPARPPPPPPPA 146
 | : | | : : : | | | | | | | | |
 Db 1555 IIADAVKEVSEMEVVTSEISEMAPQVSESTCPIPEPLADLKLPEDEDEKTPPEPEPVVPG 1614
 Qy 147 GASPLAEPAPSTPAAPKRRGSGSVDETFLFALPAASEPVIPS--SAEKIMDLMEQPGNTV 205
 | | | | | : | | | : | : | : | : | : |
 Db 1615 QVQERIPIPIEVEQAPTIPQRPPRAPKSE----LPKVAKPLDDSKSRVRFAPLNIKLGRTY 1670
 Qy 206 SSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNL SAVSSSEG TIEETLNEASKELP 265
 | | : | | | | | : : : : : : : :
 Db 1671 SEEQOK-----ELVESLE--RPLTIIT-----QQKPP 1695
 Qy 266 ERAT-----NPFVNRDLAEFSELEYSEMSSFKGSPKGESAILVENTKEEVIVRSKDKE 319
 | : | : | | | : : | | | : : | : | : |
 Db 1696 EKPTEDIGALSPLSPNTLAEYEEVPMMDM-QSVPHSP-----QEKQEEIEALSEIIE 1746
 Qy 320 DLVCSAALHSPQES-PVGKEDRVVSPEKTMDFNEMQMSVVAPVREEYADFK---PFEQA 375
 : : | | | : : : | | | | : | : | :
 Db 1747 EPQAMKEVEKPVESAPEKD NESLEAPE----IINE-----PIRRVLVETKIMGPGKSL 1795
 Qy 376 WEVKDTYPEGSRDVLAAARANVESKVDRKCLED SLEQKSLGKDS-----E 418
 | | : : | : : : : : | : : | : : |
 Db 1796 NEDNDDDDGSECLDSIGDLSERTIQR-FNTSIDDPSIRRDSFSSISSFGDRQKFR TAIE 1854
 Qy 419 GRNED-----ASFPSTPEPVKDSSRAYITCASFTSATESTT-----ANTFPLLE 462
 : | | : | | | : : | | : : : : | |
 Db 1855 NIRQDLLPFQSSVSQYL RSSNP---SQQLLVTNLSMDSPSDLSPNAPPVGFENTAQFLE 1911
 Qy 463 -----DHTSENKTDEKKIEERKAQII-----TEKTS PKTSNPF 495
 | : | | : : | | : : : : | : : :
 Db 1912 KLQQEDRPSAEGSIDSSGF EKVDHEGLDEFAAPPVHDPMQKSVFGSLGSDDMKPGSQDDG 1971
 Qy 496 LVAVQDSEADYVT-----TDTLSK-----VTEAAVSNMPEGLTPDLVQ 533
 | : : : | : | : | : : : | | :
 Db 1972 FVFIERNEANEATLKKNQKMSSHNDVIEKNYFNDNAPTAALLESPIAEEARKLVQDAVE 2031
 Qy 534 EACE-----SELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVL 588
 | | : : | : : : | | : : | | : |
 Db 2032 SASEYKKQAVDSGDEIGRELLDNVEQKIEQVKEPIVDSLHKAYDGVGDFVH-ETVPNAV- 2089
 Qy 589 PDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEAMNVALKAL 648
 | | | | | : | | : | |
 Db 2090 DDFVREAE-----KQLPESPVP----- 2106
 Qy 649 GTKEGIKEPESFNAAVQETEAPYISIIACDLIK-----ETKLSTEPSPDFSNYSEIAKFEK 703
 | | : | | : | : | : | : | : |
 Db 2107 ---EKIETPE-----PLVDIHDTVDKVHDEVNFLRREPTPPFE----- 2142

Qy 704 SVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLT---EVSETVAQHKE 760
 Db 2143 -----TDDVAPLSDDKPQFGNQTP-PE-----EDETTFDRKGPLTIPEEVEKAAAAQNN 2189

Qy 761 ERLSASPQELGKPYLESFQPNLHSTKDA-----ASNDIPTLTKKKISLQMEEFNTAI 813
 Db 2190 D-----LDDFDPLVTSNTGAAFGAAVGAAGAAVESLTEEEMFGHQ--KFETVP 2234

Qy 814 YSNDDLSSKEDKIKESETFSDSSPIEIIDFPTFVSAKDDSP--KLAKEYTDLEVSDKS 871
 Db 2235 RPPTPPKDISDEDVKPS-----TVNLGPSHHSHPSPPHHSILKHHGDAWIDFKT 2284

Qy 872 EIANIQSG-----ADSLPCLE----LPCDLSFKNIYPKDEVH 904
 Db 2285 VPPCAQNAFSPGEIMFLLAFFVYLSCFASFFSKSLPLLDNLLSLVVYLSISLI-----IH 2339

Qy 905 VSDE-----FSENRSSVSKASISPSNVSA-----LEPQTEMGSIKSKSLTKEAEK 950
 Db 2340 VKHHRKFRWNEEQATTMSKLGAVGRGLYALIAFIVNIVLRVGLNVALVVGVAVSAHEAYK 2399

Qy 951 KLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSV 1010
 Db 2400 LTKS-----SGVLRKKEVLVDVIYWRDAKSAIVLSLALLLVFLAKYPLLT 2446

Qy 1011 TAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHV 1070
 Db 2447 VTYSLLLALGAAAGFRVFKKVEAQIKKTDSEHPFSEILAQDLTLPQEKVHAQADVFEHA 2506

Qy 1071 NSTIKELRRLFLVDDLVDLSKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQ 1130
 Db 2507 TCIANKLKKLVFVESPLESIKFGVLVLSLTYSWFSGFTLAILGLLVFVSPKVIYESNQ 2566

Qy 1131 VQIDHYLGLANKSVKDAMAKIQAKIPGLK 1159
 Db 2567 EAIDPHLATISGHLKNVQNIIDEKLPFLR 2595

RESULT 6

T13564

microtubule-associated protein homolog - fruit fly (*Drosophila melanogaster*)

N;Alternate names: hypothetical protein EG:49E4.1

C;Species: *Drosophila melanogaster*

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C;Accession: T13564

R;Spanos, L.; Papagiannakis, G.; Siden-Kiamos, I.; Louis, C.

submitted to the EMBL Data Library, April 1999

A;Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.

A;Reference number: Z17689

A;Accession: T13564

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5327 <SPA>

A;Cross-references: EMBL:AL031128; PIDN:CAA20006.1

C;Genetics:

A;Cross-references: FlyBase:FBgn0025392

A;Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1

A;Note: EG:49E4.1

C;Superfamily: Drosophila 576K microtubule-associated protein homolog

Query Match 5.6%; Score 328.5; DB 2; Length 5327;
Best Local Similarity 22.7%; Pred. No. 4.1e-05;
Matches 255; Conservative 176; Mismatches 453; Indels 238; Gaps 54;

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Qy      2 EDIDQSSSLVSSSTDSPRPPPAFKYQFVTEP----EDEDEEEEEDEDEDEDELEEVL 57
      :: ||| | : ||| : | : || | | : | |
Db    3196 DEADKSKEESRRESGAEKSPLASKE--ASRPASVAESIKDEAEKSKEESRRESVAEKSPL 3253

Qy      58 ERKPAAGLSAAA--VPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAP----- 102
      | | : : | | : ||| | : || : : |
Db    3254 PSKEASRPTSVAKSVKDEAEKSKEESSRDSV--AEKSPLASKEASRPASVAESVQDEAEK 3311

Qy     103 -----ERQPSWERSPAAPAPSLPPAAVLPSKLPEDDEPPARPPPPPPAGASPLA-EPAA 156
      | : | : || | : | | : | : : | ||| : | :
Db    3312 SKEESRRESVAEKSPAYKEASRP-ASVAESIKDEAEKSKEESRRESVAEKSPLASKEAS 3370

Qy     157 PPSTPA-----APKRRGSGSVDETFLFALPAAS-EPVIPSS-AEKIMDLMEQPGNTVSSG 208
      | : | | : | | | | | | | : | | | : | |
Db    3371 RPTSVAESVKDEAEKSKEESSRDSVAEKSPLASKEASRPASVAESVQDEAEKSKEESRRE 3430

Qy     209 QEDFPSVLLETAASLPSLSPLSTVSFKEHG-----YLGNL SAVSSSEG TIEETLNEAS 261
      | | | | : | | : | : | | : : | :
Db    3431 SVAEKSPLASKEASRPASVAESVKDDAEKSKEESRRESVAEKSPLASKEASRPASVAESV 3490

Qy     262 KELPERATNPFVNRDLAEFSELEYSEMG--SSFKGSPKGESAILVENTKKEEVIVRSKDKE 319
      | : | : : || | | | : | | | : | : || : |
Db    3491 KDEAEKSKEESRRESVAEKSPGPSKEASRPTSVAESVKDEA----EKSKEE-----SRRE 3541

Qy     320 DLVCSAALHSPQES-PVGKEDRVV-SPEKTMDIFNEMQMSVAVPVREEYADFKPFEQAW 377
      : : : | : | : | | : : : : : : : | : |
Db    3542 SVAEKSSLASKEASRPASVAESVKDEAEKSKEESRRESVAEKSPLASKEAS-RPASVAES 3600

Qy     378 VKDTYEGSRDV-----LAARANVESKVDK--CLEDSL EQSLGKDSEGRNE----- 422
      || | | : | : : : || : : : : : : : | | |
Db    3601 VKDEAEKSKEVSRRESVAEKSPGPSKEASRPTSVAESVKDEADKSKEESRRESGAEKSP 3660

Qy     423 ---DASFP-STPEPVKDSSRAYITCASFTSATESTTANTFP LLEDHTS-----ENKTD- 471
      : || | | | ||| : : | | | : || | | : |
Db    3661 ASMEASRPTSVAESVKDETEK---SKEESRRESVTEKS-PLPSKEASRPTSVAESVKDE 3715

Qy     472 -EKKIEERKAQIITEKT---SPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEG- 526
      || || : : : || : | : || | | : : : : | : : |||
Db    3716 AEKSKEESRRESVAEKSPASKESSRP-----ASVAESIKDEAEGTKQESRRESMPESG 3769

Qy     527 -----LTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYP 569
      || | | : : | : | : | | : | : |
Db    3770 KAESIKGDQSSLASKETSRPDSVVESVKDETEKPEGSAL---DKSQVASRPESVAVSAKD 3826

Qy     570 TAQLCPSFEEAEATPSPVLPDIMEAPLNSLLPSAGASVVQPSVPLEAPPPVSYDSIKL 629
      | | : | | | | | | | | | : : || : | | |
Db    3827 EKSP LHSRPESVADKS---PDASKEA-----SRSLVAETASSPIEEGPRSIAD---- 3872

Qy     630 EPENPPPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIIACDLIKETKLSTEPS 689
      : : : | | : | | : : : | : : | | : |
Db    3873 -----LSLPLNLTGEAKG-KLP-TLSSPIDVAEGDFL-----EVKAESSPR 3911
```

Qy	690	PDFSNYSYEDIAKFEKSVPEH--AELVEDSSPESEPVDLF-----SDDSIPEV	733
Db	3912	P--AVLSKPAEFSQPDGTGHTASTPVDEASPVLEEIEVVEQHTTSGVGATGATAETDLLDL	3969
Qy	734	PQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDAASNDI	793
Db	3970	TETKSETV--TKQSETTLFETLTSKVESKVEVLESSV-KQVEEKVQTSVKQAETTVDLSL	4026
Qy	794	PTLTKKKIKISLQMEE-----FNTAIYSNDDLSSKEDKIKESETFSDSSP	838
Db	4027	EQLTKKS--SEQLTEIKSVLDTNISNVTNLNFSTAVETIEKKVQDVTEKVIEKAT-----	4078
Qy	839	IEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIY	898
Db	4079	-EHVSEHVT--TTGESSTETSQEKSSLDLGTFSSELRETHITTVGSPEFTV-----TIC	4128
Qy	899	PKDE--VH-VSDEFSEN----SSVSKAS-ISPSNVSALEPQTE-----MGSIVKS-	941
Db	4129	ERDEPVLHDIKEEDEEHRFSPPSDVDKAAIIPPQPMRPLSPREEEVAKIVADVAKVLKSD	4188
Qy	942	KSLT-----KEAEKKLPS--DTEKE-DRSLSAVLSAELS	972
Db	4189	KDITDIIPPDFDEROLEEKLKSTADTEEESDKSTRDEKSLEIS	4230

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Query Match          5.5%; Score 322; DB 2; Length 7962;
Best Local Similarity 21.7%; Pred. No. 0.00014;
Matches 259; Conservative 146; Mismatches 416; Indels 370; Gaps 58;

Qy          23 AFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVL-----ERKPAAGL 65
      ||: : || |: |||| |::| : | ||: |::|
Db          6574 AFEEEVVTHVEEYLVEEEEYYIHEEEEFITEEEVVPVIPVKVPEVPRKPVPEEKKPVPVP 6633

Qy          66 SAAAVPPAAA-----APLLDFSSDSVPPA-----PRGPLP-----AAP 98
      ||| |:: : ||| |::| |

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Db	6634	KKKEAPPAKVPEVPKKPPEEKVPVLPKKEKPPPAKVPEVPKKPVPEEKVPVPVPKKVEAP	6693
Qy	99	PA-APE--RQPSWERSPAAPAP---SLPPA-AAVLPSKL-PEDDEP---PAR---PPPPP	144
Db	6694	PAKVPEVPKKPVPEKKVPVPAPKKVEAPPAKVPEVPKKLIPEEKKPTVPVPKKVEAPPPKV	6753
Qy	145	PAGASPLAEPAPPPSTPAAPKRRGSGSVDETLFALPAASEVPVPSSAEKIMDLMEQPGNT	204
Db	6754	PKKREPVPVPVALPQE-----EEVLF-----EEEIVPE--EEVLPEEEEE----	6790
Qy	205	VSSGQEDFPSVLLETAASLP---SLSPLSTVSFKEHGYLGNLSAVSSSEGTI--EETLNE	259
Db	6791	VLPEEEEE--VLPEEEEEVLPEEEEEIPPEEEVPPEEEY-----VPEEEEFVPEEEVLPE	6841
Qy	260	ASKELPERATNPVNRDLAEFSELEYSEMGSSEFKGSPKGESA-----ILVENTKEEVIV	313
Db	6842	VKPKVPVPAPVPEIKKKVTEKKVV-----IPKKEEAPPAKVPEVPKKVVEEKRII	6890
Qy	314	RSKDKEDLVCSAALHSPQESPVGKED-----RVVSPEKTMDFNEM-----	354
Db	6891	LPKEEEVLPEVVT-EEPEEEPISEEEIPEEPPSIEEVEEVAPPRVPEVIKKAVPEAPTPV	6949
Qy	355	-----QMSVVAPVREEYADFKPFQAWEVKDTYEGSRDVLAAARANVESK	398
Db	6950	PKKVEAPPAKVSKKIPEEKVPVPVQKKEA---PPAKVPEVPKKVPEKKVLVPKKEAVPPA	7006
Qy	399	VDRKCLEDSEADYVTTDTLSKVTEAAV-----SNMPEGLTPDLV-----	532
Db	7007	KGRTVLEEKVSVAFRQEVVVKERLELEVVEAEVEEIPEEEEFHEVEE-----YFEEG	7058
Qy	445	SFTSATESTTANTFPLLEDHTSEN-----KTDEKKIEER-----KAQIITEKTSPT	491
Db	7059	EFHEVEEFIKLEQHRVEEEHRVEKVRVIEVFEEAEVEVFKEPKAPPKGPEISEKIIPPK	7118
Qy	492	SNPFLVAVQDSEADYVTTDTLSKVTEAAV-----SNMPEGLTPDLV-----	532
Db	7119	KPPTKVVPKPEPPPAKVPEVPKKIVVEEKVRVPEEPRVPPTKVPEVLPPKEVVPEKKVPVP	7178
Qy	533	----QEACESELNEATGTKIAYETKVDL-----VQTSEAIQESLYP	569
Db	7179	PAKKPEAPPPKVPEAP-KEVVPEKKVPVPPPKKPEVPPTKVPEVPKAAVPEKKVPEAIPP	7237
Qy	570	TAQLCPS--FEEAEATPS-----PV-LPDIOMEAPLNSLLPSAGASVVQPSVSPL	617
Db	7238	KPESPPPEVFEEPEESPSAPPKKPEVPPVRVPEVPKEVVPEKKVPAAPPK--KPEVTPVK	7295
Qy	618	AP-----PPVSY-----DSIKLEPENPPP--YEE	639
Db	7296	VPEAPKEVVPEKKVPVPPPKKPEVPPTKVPEVPKVAVPEKKVPEAIPPKPESPPPEVFEE	7355
Qy	640	AMNVALKALGTKEGIKEPESFNAA-----VQETEAPYISACDLIKETKLSTEP	688
Db	7356	PEEVALEE-PPAEVVEEPEP--AAPQVTVPPKNPVPEKKAPAV-----VAKKPELPPVK	7407
Qy	689	SPDFSNYSEIAKFESVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESL	748
Db	7408	VPEVP--KEVVP-EKKVP----LVVPKKPEAPPA-----KVPEVP-----KEVV	7444

RESULT 9

A47283

calphotin - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000

C;Accession: A47283

R;Ballinger, D.G.; Xue, N.; Harshman, K.D.

Proc. Natl. Acad. Sci. U.S.A. 90, 1536-1540, 1993

A;Title: A *Drosophila* photoreceptor cell-specific protein, calphotin, binds calcium and contains a leucine zipper.

A;Reference number: A47283; MUID:93165730; PMID:8434015

A;Contents: photoreceptor cells

A;Accession: A47283

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-873 <BAL>

A;Cross-references: GB:L05080; NID:g157071; PIDN:AAA28420.1; PID:g157072

A;Note: sequence extracted from NCBI backbone (NCBIN:124958, NCBI:124959)

C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; von Willebrand factor type C repeat homology

Query Match 5.2%; Score 304.5; DB 2; Length 873;
Best Local Similarity 21.9%; Pred. No. 3.1e-05;
Matches 213; Conservative 126; Mismatches 362; Indels 273; Gaps 42;

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Qy      62 AAGLSAAVPPAAAPLLDFSSDSVPPAPR--GPLPAAP----PAAP-----ERQPSWER 110
      :|::|  | | ||:  | :|  |  | |||  | ||  ||:
Db      11 SAPVAAPVTPSAVAAPVQVVSAAVAVAPAVVAPAPAAPTAVTPVAPPPTLASVQPATVT 70

Qy     111 SPAAPAP----SLPPAAVLPSKLPEDDEPPARPPPPPP-----AGASPLAEPAAAP 158
      | |||  |: | |:| | :  | | |  ||  |:::| | |
Db      71 VP-APAPIAAASVAPVASVAPPVVAAPTTPAASPVSTPPVAVAQIPVAVSAPVAPPVAAT 129

Qy     159 STPAAPKRRGSGSVDETFLALP--AASEP----VIPSSAEKIMDLMEQPGNT--VSSGQ 209
      || |  | : | | || |  | | : |  | |  |::
Db     130 PTPVAPI-----PVAAPVIATPPVAASAPTPAAVTPVVSPIATPPVVPANTTVPVAAPV 184

Qy     210 EDFPSVLLETAASL-PSLSPLSTVSFKEHGYLEGNLSAVSSSEGTTIEETLNEASKELPERA 268
      |: :  | | |::|  |  :: :  || | :  |: |
Db     185 AAVPAAPVVPVAPVLAPAVAPAVAPVVAETPAPPPVAEIPVA--TIPECVAPLIPEVSVVA 242

Qy     269 TNPFFVNRDLAEFSELEYSEMGSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALH 328
      | |  | | : |  | | : |
Db     243 TKPLA-----AAEPVVVAPPATETPVVAPAAA 269

Qy     329 SPQESPVGKEDRVVSPEKTMDFNEMQMSVAPVREEYADFKPFQAWVEVKDITYEGSRDV 388
      || |  |:|  ::: ||||
Db     270 SPHVS-----VAP-----AVETAVVAPV----- 287

Qy     389 LAARANVESKVDRKCLEDSEQLKSL----GKDSEGRNEDASFPSTPEPVKDSSRAYITCA 444
      |: |  | : | :  :  | : | | | : :
Db     288 ---SASTEPPVAAATLTAPETPALAPVVAESQVAANTVVATPPTPAPEPETIAPPVVAE 344

Qy     445 SFTSATESTTANTFPLLEDHTSENKTDEKKIEERKAQIITEKTSPKTSNPFLVAVQDSEA 504
      :  |: :  | |::  :|:  |  | | : | | :

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Db	345	TPEVASVAVAETTPPVVPPVAAES-----IPAPVVATTPVPATLAVTDPD-	389
Qy	505	DYVTTDTLSKVTEAAVSNMPEGLTPDLVQEQACESELNEATGTKIAYETKVLDLVQTSSEAIQ	564
		: : :	
Db	390	-----VTASAVPELPPVIAPSPVPSA-----VAETPVDLA-----P	420
Qy	565	ESLYP-TAQLCPSF--EEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAP--	619
		: : : : : : : : :	
Db	421	PVLPPVAAEPVPAVVAEETPETPAPASAPVTI-AALD--IPEVAPVIAAPSDAPAEAPSA	477
Qy	620	--PPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACD	677
		: : : :	
Db	478	AAPIVS-----TPPT-----TASVPETTAPPAAVPTE	504
Qy	678	-----LIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAE--LVEDSSPESEPVDLFSD-DS	729
		: : : : : : : : : :	
Db	505	PIDVSVLSEAAIETPVAPPVEVTTEVAVADVAPPEAAEDLIEPVEPPAPIPDLLEQTTS	564
Qy	730	IPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDAA	789
		: : : : : : : : : : : : : :	
Db	565	VPAVEAAESTSSPIPETSLPPPNEAVA--SPEVAVAPITAPEPIPEP-EPSLATPTEPI	620
Qy	790	SNDIPTLTKKKIKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSOSSPIEIIDEFPTFV	849
		: : : : : : :	
Db	621	PVEAPV-----VIQEAVDAVEVPVTETSTSIPETTVEFPEAV	657
Qy	850	SAKDDSPKLAKEYTDLEV-SDKSEIANIQSGAD----SLPCLELPCDLSFKNIYPKDEVH	904
		: : : : : : : : :	
Db	658	AEKVLDPAI----TEAPVTTQEPDVANINDGAPATEITTPAVEI-----VT	699
Qy	905	VSDEFSENRRSSVSKASISPSNVSALE-PQTEM--GSIVKSKSLTKEAEKKLPSDTEKEDR	961
		: : : : : : : : : : : : :	
Db	700	AAAEVSDTAIPLIDPPV-PQEIABAEIPETETKPAEVIVEQS-TIPIEAPVPEVSKYAEP	757
Qy	962	SLSAVLSAELSKTS	975
		: : : :	
Db	758	VISEAPAAEVRITA	771

T24583

C;Species: *Caenorhabditis elegans*

C;Accession: T24583

submitted to the EMBL Data Library, April 1995

A;Accession: T24583

A;Molecule type: DNA

A;Cross-references: EMBL:Z49130; PIDN:CAA88964.1; GSPDB:GN00020; CESP:T06D8.1

A;Experimental source: clone T06D8

C; Genetics:

A; Gene: CESP:T06D8.1

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A;Map position: 2
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A;Introns: 1391/3; 1432/3; 1470/3; 1505/1; 1520/1; 1616/1; 1644/1; 1687/3;
1742/1

Query Match 5.2%; Score 302.5; DB 2; Length 1829;
Best Local Similarity 21.1%; Pred. No. 0.00011;
Matches 233; Conservative 157; Mismatches 469; Indels 245; Gaps 38;

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Qy      2 EDIDQSSLVSSSTDSPPR-----PPPAFKYQFVTEPEDEE-----DEEEE-----E 42
      |:  ::| || : |      |      | |||  ||      :  ||      |
Db      212 EETTVVAVVESSGEEPASSSTSIPTELSKNDQVTEASGEETITAAATEASEETTTSAVTE 271

Qy      43 DEEEDDEDLEELEVLERKPAAGLSAAAVPPAAAAPLLDFFSSDSVPPAPRG---PLPAAPP 99
      ||  :  ::| :||:  |: ::|      :  ||  |      ||
Db      272 GSGEDTTVVAVVELSGEQPAS--SSTSIP-----TELSKDDQVTEASGEETTTAAATE 322

Qy     100 AAPERQPS-----WERSPAAPAPSLPPAAAVLPSKLPEDDE-PPARPPPP 143
      |: |  |      | |  || |  :  ::|:| :||:  |
Db     323 ASEETTTSAVTEGSGEETTVVAVVESSGEEPASS---STSIPTELSKDDQVTEASGEET 378

Qy     144 PPAGASPLAEPAAPSTPAAPKRRGSGSVDETLFAL-----PAASEPVIPSSAEKIMD 196
      | |:  :|      | :  |||  | |:  |      ||:|  ||:  |
Db     379 TTAAATEASE-----ETTTSVTEGSGE-DTTVVAVVESSGEGQPASSSTSIPTELSKDDQ 432

Qy     197 LMEQPGN-----TVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEH 237
      :  |  |      | ||:  :  ::|:  |:  |  |  :
Db     433 VTEASGEETTTAAATEASEETTTSAVTEGSGEDTTVVAVVESSGEGQPASSSTSIPT---- 488

Qy     238 GYLGNL SAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSEFKGSPK 297
      |      |:  :|  |||  |:  |  |  |  |      |:  :  :  ||:
Db     489 -ELSKDDQVTEASG--EETTTAAATEASEETTTSAVTEGSGEETTV-VAVVESSGEEPAS 544

Qy     298 GESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPV-----GKEDRVVSPEKTM DI 350
      ::|  | :|:  :  :  :|  :|  | :|:  | :|  ||:  ::|
Db     545 SSTSIPTELSKDDKVTEASGEETTTAAATDASSEETTTSAVTEGSGEETTVVAVVESSD- 603

Qy     351 FNEQMMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLED SLEQ 410
      |  |  :  |  | :  | :|  |      ||  |      |||:
Db     604 -EEPASSSTSIPTELSKDDQVTEASGEETTT-----AAATEASEETTTSAVTEGSGEE 655

Qy     411 KSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKT 470
      ::  |  |:  :  ||  | :  |  :|  |  | :|||  :  |:  :
Db     656 TTVVAVVESSGEEPASSSTSIPTELSKDDKVTEA---SGEETTTAAATDASSEETTTSAV 712

Qy     471 DEKKIEERKAQIIITEKTSKP-TSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTP 529
      |  ||      :  |:  :  |:  :  :|:  ||  :  :  ||:  |  |
Db     713 TEGSGEETTVVAVVESSDEEPASSSTSIPTELSKDDQVTEASGEETTTAAATEASEETTT 772

Qy     530 DLVQEACESELN-----EATG-----TKIAYETKVDLVQTSEAIQESLYPTAQLCPSF 577
      |  |  |      |:  |  ||  |  |  | :||  |  |  :
Db     773 SAVTEGSGEETTVVAVVESSGEEPASSSTSIPTELSKD-DQVTEASGEE---TTTAAATE 828

Qy     578 EEAEATPSPVLPDIMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPY 637
      |  |  |  :  :  ::| :|  ||:  |  |  :|
Db     829 ASEETTTSAVTEGSGEDTTVVAVVESSGE---QPASSSTSIPTELS----- 871

Qy     638 EEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSE 697
      |:  :  |:  :||  :  | :  :||  |      :
```

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Db      872 -----KDDQVTEASGEETTT---AAATEASEETTTSAVTEGSGEETTV 911
Qy      698 IAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEV---PQTQEEAVMLMKESLTEVSET 754
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      912 VAVVSSGEEPA-----SSSTSIPTELSKDDQVTEASGEETTTAAATEASSEETTTSAVT 966
Qy      755 VAQHKEERLSASPQELGKPYLESFQP-----NLHSTKDAASN----- 791
      :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      967 EGSGEETTTSAVTEGSGEETTTSAVPEGENSTTEAPAFVTGSEIEIPSSSESSSTTHDP 1026
Qy      792 DIPTLTKKKIKISLQMEEFNTAIYSNDDLSSKEDIKIKESFSDSSPIEIIDFPTFVS 850
      || :| | | :| :| : | : : : | | : | : | | | | | | |
Db      1027 SIPVITPKPSVSSSTIENVMSKTSSEE---AAEKKIIGEHQTKGDDAGKEDEDNMPAFVT 1083
Qy      851 A-----KDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCD 891
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1084 ANPAGTSTTESAENVSTSTGEEDENIKMAKELGKQFAADLAKLA----- 1126
Qy      892 LSEFKNIYPKDEVHVSDEFSENSSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKK 951
      || | : : | : : | | : | | : | | : : | | : : | | : :
Db      1127 -----AKDGVNLT-ETADAKDSGETAHVEDEQVSSSTE--SSIGSEETTTTVNKETTEE 1176
Qy      952 LPDTEKEDRSLSAVLSAELSKTS 975
      : : | | : : | | | | | | | | | | | | | | | | | |
Db      1177 HHEASGEEDDAPAFVTGAPTDSTT 1200

```

RESULT 11

A47282

calcium-binding protein calphotin - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C;Accession: A47282

R;Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A.

Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1993

A;Title: Calphotin: a *Drosophila* photoreceptor cell calcium-binding protein.

A;Reference number: A47282; MUID:93165729; PMID:8094559

A;Accession: A47282

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-865 <MAR>

A;Cross-references: GB:L02111; NID:g157031; PIDN:AAA28405.1; PID:g157032

A;Experimental source: photoreceptor cells

A;Note: sequence extracted from NCBI backbone (NCBIN:124955, NCBIP:124956)

C;Genetics:

A;Gene: FlyBase:Cpn

A;Cross-references: FlyBase:FBgn0010218

C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; von Willebrand factor type C repeat homology

C;Keywords: calcium binding

Query Match 5.1%; Score 295.5; DB 2; Length 865;

Best Local Similarity 21.3%; Pred. No. 7.2e-05;

Matches 217; Conservative 127; Mismatches 379; Indels 295; Gaps 41;

```

Qy      62 AAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPER----QPSWERSPAAPAP 117
      :| ::| | | ||| : | :| ||| | : | | | | | : | |||

```

Db 11 SAPVAAPVTPSAVAAPVQVVSPAAPVAPAPAAPIAVTPVAPPPTLASVQPATVTIP-APAP 69
 Qy 118 ----SLPPAAAVLPSKLPEDDEPPARPPPPPPAGA-----SPLAEPAAPSTP----- 161
 | : | | : | : | | | | | : | : | | | |
 Db 70 IAAASVTPVASVAPPVVAAPTPPAASPVSTPVAVAQIPVAVSAPVAPPVAATPTPVVQIP 129
 Qy 162 -AAPKRRGSGSVDETLFALP--AASEP----VIPSSAEKIMDLMEQPGNT---VSSGQED 211
 | | | : | | | | | | : | | | | : :
 Db 130 VAAP-----VIATPPVAASAPTPAAVTPVISPVIASPPVVPANTTVPVAAPVAA 178
 Qy 212 FPSVLLETAASL-PSLSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATN 270
 | : : | | | : : | : : : | | | : | : | |
 Db 179 VPAAVPVVAAPVLAPAVAPAVAPVVAETPAPPPVAEIPVA--TIPECVAPLIPVSVVATK 236
 Qy 271 PFVNRDLAEFSELEYSEMGSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSP 330
 | | | | | | | : | | | : | | | |
 Db 237 PLA-----AAEPVVVAPPATETPVVAPAAASP 263
 Qy 331 QESPVGKEDRVVSPKTMDFNEMQMSVAPVREEYADFKPFQAWKDYEGSRDVL 390
 | | | : | : : : | | | |
 Db 264 HVS-----VAP-----AVETAVVAPV----- 279
 Qy 391 ARANVESKVDKCLEDSLEQKSL----GKDSEGRNEDASFPSTPEPVKDSRAYITCASE 446
 | : | | | : | : | : | : | | | : : :
 Db 280 -SASTEPPVAAATLTAPETPALAPVVAESQVAANTVVATPPTPAPEPETIAPPVVAETP 338
 Qy 447 TSATESTTANTFPILLEDHTSENKTDEKKIEERKAQIITEKTSPKTSNPFLVAVQDSEADY 506
 | : : | | : : : | | | | : | | :
 Db 339 EVASVAVAETTPPVVPVAAES-----IPAPVVATTPVPATLAVTDPD--- 381
 Qy 507 VTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVLDLVQTSEAIQES 566
 | | : | | : | | | | | | | |
 Db 382 -----VTASAVPELPPVIAPSVPSA-----VAETPVDLA-----PPV 414
 Qy 567 LYP-TAQLCPSPF--EEAEATPSVPLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAP---- 619
 | | | : | : | | : : | : : | : | | | |
 Db 415 LPPVAAEPVPAVVAETPETPAPASAPVTI-AALD--IPEVAPVIAAPSDAPAEAPSAAA 471
 Qy 620 PPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACD-- 677
 | | | | | | | : | | | | : : :
 Db 472 PIVS-----TPPT-----TASVPETTAPPAAVPTEPI 498
 Qy 678 ---LIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAE--LVEDSSPESEPVDLFSD-DSIP 731
 : : | : | : | : | : : | | : | | : | |
 Db 499 DVSVLSEAAAIETPVAPPVEVTTEVAVADVAPPEAAADLIEPVEPPAPIPDLLEQTTSVP 558
 Qy 732 EVPQTQEEAVMLKESLTVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDAASN 791
 | : : : : | | : | | : : | : | : | : :
 Db 559 AVEAAESTSSPIPETSLPPPNEAVA---SPEVAVAPITAPEPIPEP-EPSLATPTEPIPV 614
 Qy 792 DIPTLTKKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDFPTFVSA 851
 : | : : | : : | : : | : : | | | | :
 Db 615 EAPV-----VIQEAVDAVEVPVTETSTSIPETTVEFPEAVAE 651
 Qy 852 KDDSPKLAKEYTDLEV-SDKSEIANIQSGAD----SLPCLEL-----PCDLSFKNIYP- 899
 | | : | : : : : | | : | : | : : | |
 Db 652 KVLDPAI---TEAPVTTQEPDVANINDGAPATEITTPAVEIVTAAAEVSDIAIPVIDPP 707

Qy 900 -KDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMG----- 936
 | : | : | : : : | : | :
 Db 708 VPQEIAVA-EIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAAEVPITAGDN 766
 Qy 937 ----SIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGV 990
 | : | : : ||| : | | : | : : || || : | |
 Db 767 PDNTSVGISEVVPTIAEKPVVEEVPSTSEIPEQSSSPSDSVPVAKITPLL--RDLQTTDV 822

RESULT 12

T34513

hypothetical protein ZK783.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T34513

R;Favello, A.; Vaudin, M.

submitted to the EMBL Data Library, August 1994

A;Description: The sequence of *C. elegans* cosmid ZK783.

A;Reference number: Z21536

A;Accession: T34513

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-3507 <FAV>

A;Cross-references: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783.1

A;Experimental source: strain Bristol N2; clone ZK783

C;Genetics:

A;Gene: CESP:ZK783.1

A;Map position: 3

A;Introns: 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1;
 1409/2; 1450/1; 1760/1; 1898/1; 2153/1; 2628/1; 2681/1; 2899/1; 2946/1; 3088/3;
 3184/1; 3283/1; 3346/3; 3365/3; 3484/3; 3504/1

Query Match 5.0%; Score 292; DB 2; Length 3507;

Best Local Similarity 20.6%; Pred. No. 0.00072;

Matches 226; Conservative 146; Mismatches 491; Indels 236; Gaps 37;

Qy 11 SSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDL--EELEVLERKPAAGLSAA 68
 |||::| || : :|| : :|| | | : || | : |
 Db 2043 SSSSEAPLTSSPATTTEVITESSVKSTTPKEESSSEITVKLSSKSPEVTESSVKSSPSTP 2102
 Qy 69 AVPPAAAAPLLDFSSDSVPPAPRGPLPAAPP----AAPERQPSWERSPA-----APAPSL 119
 : : : :| | : | : : | : | :| | : ||
 Db 2103 STTSQSVTSTVPETSKSTVLSSEAPVTSTSPTEVHTSSETKPPLSASSTTGDTNSTTPST 2162
 Qy 120 PPAAAVLPSKLPEDDEPPARPPPPPPAGASP-LAEP-----AAPPSTPAAPKRRGSGSV 172
 | : | : || | | : || : :| | || | : ||
 Db 2163 SSLASVKSTSAPEGTS--ASVAPVKLSSSLSPDVSQPSTKTFDATESSTVQASETSSGTSV 2220
 Qy 173 DET-----LFALPAASEPVI-PSSAEKIMDLMEQPGNTVSSGQEDFP----SV 215
 | : : :| | | | : : ||| :| ||| | |
 Db 2221 KSTSEPESHVTKLSITSSNPSSSVPVTSKSTPTVPESTEQPTSTTPSGQSLTPMNSNSE 2280
 Qy 216 LLETA---ASLPSLSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERAT--N 270
 : | : ||| : | | | : : : | :| | :
 Db 2281 VLTSEPHVLSSSLSPDVSQSSTTPNNLSESSTVETPKTSSEVSLNSEEPSTTEAPTTL 2340

Qy 271 PFV---NRDLAEFSEL---EYSEMGSSFKGSPKG-----ESAILVENTKEEVIVRSKD 317
 | : : : : | : : | : | : | : : : | : :
 Db 2341 PDILSTTTNNLSQSSTVSTEDRSEISSENSEKPTSAPELVTSSVTHVASSSPDVPTESSE 2400

 Qy 318 KEDLVCSAALHSPQ-----ESPVGKEDRVVSPEKTMDFNEMQMSVAVPREEYADFK 370
 : || | : : : | : : | : | : : | : | :
 Db 2401 PDDLTSSTENIPEASSKQTISSTPTPDTTASEEPTKSTSMSPDLSTTSNVLSSESSTTP 2460

 Qy 371 PFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLEDSEQKSLGKDSEGRNEDASFPSTP 430
 | : || : : || : || : || : || : || : ||
 Db 2461 ESSSKSPVSSSTEG---ISVVTSTEFKSKVPESTISSVLE-----EDLT-KTTP 2504

 Qy 431 EPVKDSSRAYITCASFTSAT-----ESTTANTFPLLEDHTSENKTDEKKIEE 477
 | : : : | || || | || : | : : : | :
 Db 2505 SPILEET----TTASETSEPLTEDSLTVSVRIHELTTSSENVPKSESTTTSSSESKPSQ 2560

 Qy 478 RKAQIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGL-----TPDLV 532
 | | : | || : | : : || : || : | : | : |
 Db 2561 EPAGILTSTVVPTSSVSLITASEIEA--ITSNTPFKQGRTPITTSKSLVKSTTSPSTV 2618

 Qy 533 --QEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPD 590
 | || | : : | : || : : | : | : | : : |
 Db 2619 TSSEPSESTKRRTTVSTTVSTTTPTTEETTTSESLILTAAPSK---PTESTTESSEAPTTP- 2674

 Qy 591 IVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGT 650
 | | : || : || : : : || : : :
 Db 2675 -----AKTSETKPS-----NVSSTSRKS 2692

 Qy 651 KEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAE 710
 | : : | : : : : | || | : : : | | |
 Db 2693 TENVETSTSQSGSLESS-----TMSSTSSEPETNAPAVTVSSEASSTTLEE 2738

 Qy 711 LVEDSSPESEPVDFLSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKE-ERLSASPQE 769
 ||| | : || ||| : : | : : | : | : | : |
 Db 2739 NSSTSSPTSSEASVKLSSLFPE--SITSEAVTVSSRAPAEITMSSESHREISTVSSEPSE 2796

 Qy 770 LGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSS----- 822
 | : || : : | : | : | : | : | : ||| :
 Db 2797 PEIPLSTTVSPNVVTASSIPSEE-PILSSVTSSSTPRVRLITG--TPDDLIVSVTVPSHG 2853

 Qy 823 -KEDKIKESETFSDS-SPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGA 880
 : | | | : | ||| : | | : || | ||
 Db 2854 NRRQNITASSVPSNSTSPIILPSESLTTPQPPPTTTTAKPAT-----TSGK 2900

 Qy 881 DSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVK 940
 | : : | : : : | || | |
 Db 2901 RGPPSIQPPAEM-----FTTPAPPPPSNGGYGEE----- 2929

 Qy 941 SKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLL 1000
 | : | : : | | | || : : : | : || | :
 Db 2930 ----TNQEEEQVTSTTTTEAPSLCSTVTCHSLATCE-----QSTGVCICRDGFID 2976

 Qy 1001 SLTVFSIVSVTAYIALALL 1019
 | | | | : | |
 Db 2977 GTTACSKKSTADCISLPSL 2995

RESULT 13

A56577

microtubule-associated protein MAP 1B - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 16-Feb-1997

C;Accession: A56577

R;Zauner, W.; Kratz, J.; Staunton, J.; Feick, P.; Wiche, G.

Eur. J. Cell Biol. 57, 66-74, 1992

A;Title: Identification of two distinct microtubule binding domains on recombinant rat MAP 1B.

A;Reference number: A56577; MUID:92347374; PMID:1639092

A;Accession: A56577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2364 <ZAU>

A;Cross-references: GB:X60550

A;Experimental source: brain

A;Note: nucleotide sequence not given; conceptual translation not complete

C;Superfamily: microtubule-associated protein MAP1B

Query Match 5.0%; Score 291.5; DB 2; Length 2364;
Best Local Similarity 20.0%; Pred. No. 0.00043;
Matches 220; Conservative 167; Mismatches 456; Indels 255; Gaps 44;

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Qy      30 TEPEDDEDEEEEEDEEEDDEDLEELVLERKPAAGLSAAAVPPAAAAPLLDFFSSDSVPPA 89
      :| | ||:|:: || |:: : :: | | | | | : : | :
Db      913 SEEEGEEEEEDKAEDAREEDHEPDKTE-----AEDYVMAVVDKAAEAGVTEDQYDFL--- 963

Qy      90 PRGPLPAAPPAAPERQPSWERSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPPAGAS 149
      | :| | :|| ||::: || | | | |
Db      964 -----GTPAKQ-----PGVQSPSREPASSIHDETLPGGSESEAT-----AS 999

Qy     150 PLAEPAAPSTPAAPKRRGSGSVDETLEFALPAASEPVIPSSAEKIMDLMEQPGN---TVS 206
      | | | | | | : ||| | :| | | |
Db     1000 DEENREDQPEEFTAT----SGYTQST---IEISSEPTPMDEMSTPRDVMTDETNEETES 1052

Qy     207 SGQE-----DFPSVLLETAASLP---SLSPLS----TVSFKEHGYLGNL SAVSSSEG TIE 254
      || : | | | | : || | : | : | : |
Db     1053 PSQEFVNITKYESSLYSQEYSKPVVASFNGLSDGSKTDATDGRDYNASASTISPPSSMEE 1112

Qy     255 ETLNEAS-----KELPERATNPFVNRDLAEF--SELEYSEMG--- 289
      : :::: |:: : :| : :| : | : :|
Db     1113 DKFSKSALRDAYRPEETDVKTGAELDIKDVSDERLSPAKSPSLSPSPSPSPIEKTPLGERS 1172

Qy     290 -----SSFKGSPKGESAILVENTKEEVIVR----SKDKEDL-----VCSAALHSP 330
      : | | :||: :| : :| | ::: | | :| | :|
Db     1173 VNFSLTPNEIKASAEGEATAVVSPGVTQAVVEEHCASPEEKTLEVVSPSQSVTGSAGHTP 1232

Qy     331 -QESPVGKEDRVVSPEKTMDIFNEMQMSVVAPVREEYADFK-----PFEQAWEVKD 380
      :|| :: : | | : : || | : : | | : : | |
Db     1233 YYQSPTDEKSSHLPT EVT-----ENQAVPVSFEFTEAKDENERSSISPMDE--PVPD 1283

Qy     381 TYEGSRDVLAARANVESKVDRKCLED--SLEQKSLGKDS----EGRNEDASFPSTPEPVK 434
      : ||: : || | : | :||: | | ||
Db     1284 SESPIEKVLSPLRSPPLIGSESAYEDFLSADDKALGRRSES PFEGKNGKQGFS DKESPV S 1343

Qy     435 DSSRAYITCASFTSATESTTANTFPLLEDHTSENKT-----DEKKI----- 475

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      |      :|      :      |      |      | : || : | |      ||:|:
Db    1344 D-----LTSDLYQDKQEEKRAGFIPIKEDFSPEKKASDAEIMSSQSALALDERKLGGDGS 1398
Qy    476 -----EERKAQIITEKTSKPTSNPFLVAVQDSEADYVTTDTLSKVTEAAV-- 520
      | : | |      | :|: |      :|: |      : : : | : | :|
Db    1399 PTQVDVSQFGSKFEDTKMSISEGTVSDKSATPVDEGAEDT---YSHMEGVASVSTASVAT 1455
Qy    521 SNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQES-LYPTAQLCP---S 576
      | : || | | | : :|: | :|: | :||| ||: : | : : || |
Db    1456 SSFPEPTTDD-VSPSLHAEVGSHPSTEVDDSLSVSVVQTPTTFQETEMSPSKEECPRPMS 1514
Qy    577 FEEAEATP-----SPVLPDIVMEAPLNSLL-----PSAGASVVQ 610
      : :|      | : : | :| :||      | : || : :
Db    1515 ISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSLAMDFSRQSPDHPTVGAGMLH 1574
Qy    611 PSVSPLEAPPPVSYD-----SIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFN 661
      : : | | | | :|: | | | : : : : : | : :
Db    1575 ITEN---GPTEVDYSPSDIQDSSLHKIPTEEPSYTQDNDLS-ELISVSQVEASPSTSS 1630
Qy    662 AAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESEP 721
      |      || | :| | | | :|: | : | :| ||:|:
Db    1631 AHTPS-----QIASPLQEDTLSDVVPDRMSLYASLASEKVQSLEGEKL----SPKSDI 1680
Qy    722 VDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYL-ESFQP 780
      | :| |      : : ||| | :| : : :| | | : : |
Db    1681 SPLTPRESSPTYSPGFSDSTSGAKES-TAAYQTSSSPPIDAAAAEPYGFRSSMLFDTMQH 1739
Qy    781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE 840
      :| :| : : : :|: | :| | : | : : : | | | :
Db    1740 HLALSRDLTTSSV----EKDNGGKTPGDFNYAYQKPESTTESPDEEDYDYE--SHEKTIQ 1793
Qy    841 IIDEFPTFVSAKDDSPK----LAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKN 896
      | : : : :| | :|: | : | : | | | : : |
Db    1794 AHDVGGYYYEKTERTIKSPCDSGYSYETIEKTTKTP----EDGGYS-----CEITEKT 1842
Qy    897 IYPKDEVHVSDEFSENRSSVSKAS-----ISPSNVSALEPQTEMGSIVKSKSL 944
      :| | | || : : | : : : : : | : |
Db    1843 TRTPEEGGYSEISEKTTTRTPEVSGYTYEKTERRRLLDDISNGYDDTEDGGHTLGDCSY 1902
Qy    945 TKEAEKKLPSDTEKEDRS 962
      : | :|: | | | |
Db    1903 SYETTEKITSFPESESYS 1920

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RESULT 14

T19431

hypothetical protein C25A1.10 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C;Accession: T19431

R;Mortimore, B.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19124

A;Accession: T19431

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-971 <WIL>

A;Cross-references: EMBL:Z81038; PIDN:CAB02755.1; GSPDB:GN00019; CESP:C25A1.10
A;Experimental source: clone C25A1
C;Genetics:
A;Gene: CESP:C25A1.10
A;Map position: 1
A;Introns: 38/3; 92/3; 201/3; 919/3
C;Superfamily: nucleolus-cytoplasm shuttle phosphoprotein

Query Match 4.9%; Score 288.5; DB 2; Length 971;
Best Local Similarity 20.6%; Pred. No. 0.00016;
Matches 198; Conservative 127; Mismatches 391; Indels 247; Gaps 35;

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Qy      7 SSLVSSSTDSPRPPPAFKYQFVTEP---EDEEDEEEEEEEEEDEDEDLEELEVLERKPAA 63
      || || || ||: || : : : : : || : : : ||
Db     147 SSSDSDSDDEPPKKAPAVTTKVAPKPMKKQDTSDDSDSDSESDSDGKSKKANPVKVTPVA 206

Qy     64 GLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAP-----ERQPSWE 109
      : | | ||: || | || : | || | | | | : || :
Db     207 NVLQKVVAKKAASSSSDSSDDEKKPAK-PTPAKPTPKPVVKAESSSDSSDDEKKPVAK 265

Qy    110 RSPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRGS 169
      :|| | | | | | ||| ||: | | | :|: | | : : :
Db    266 PPAKATPK-PAKKADSSSDSSDDEAPAK-KTPAKAAPKPVAKKAESSSDSSDDEKK-- 321

Qy    170 GSVDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPL 229
      ||| | : | : : : : | : | : : | : : | :
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Qy    230 STVSFKEHGYLGNL SAVSSSEG TIEETLNEASKELPERATNPFVNRDLAEFSELEYSE-- 287
      : | | | : : : | : | | : | | | : | : |
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Qy    288 ---MGSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSP 344
      : | | : || : | | | : : | | : | | : |
Db    415 PVAKPTSATKATPK-----PAKKAD---SSSDSSDDEAPAKKTPAKAAP 455

Qy    345 E---KTMDIFNEMQMSVVPVREEYADFKPFEQAWVKDITYEGSRD-----VLAARANV 395
      : | : : : : | | | : | : | | | | |
Db    456 KPASKKAESSSDSSDDEKPAKSTPAKITPKPTAKKVASSSDSSDDEKKPAKPTPANA 515

Qy    396 ESKVDRKCLEDL-----EQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSAT 450
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Db    516 TPKPVAKKAESSSDSSDDEKKPVAKPTSAT-----ATPKPAKKADLSSDFSDDDEAPA 568

Qy    451 ESTTANTFPLEDHTSENKTDEKKIEERKAQIITEKTSPK-TSNPFLVAVQDSEADYVTT 509
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Db    569 KKTPAKAAPKPAKKAESSSDSSDDEKPAKSTPAKTPKPTAKKAASSSDSSDDEK--EK 626

Qy    510 DTLISKVTEAAVSNMPEGLTPDLVQEACESELN-----EATGTKIAYETKVDLVQTSEAI 563
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Db    627 KPVAKPTSATKATPKPAKKADSSSDSSDDEAPAKKTPVKPTPVKIVAK-KVD--SSSDSS 683

Qy    564 QESLYPTAQLCPSFEEAEATPSPVLPDIMEAPLNSLLPSAGASVVQPSVSPLEAPPPVS 623
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Qy    624 YDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIIACDLIKETK 683

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Db	711	SDS--SDDEKKPVVKQTPNVV-----PKKEKAASSSDSS-----DDEKK	748
Qy	684	LSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESEPVDFSDDSIPEVPQTQEEAVML	743
Db	749	PTAKPTP-----KATPKQSAKKADSSDDS-----SDDEAPA-----	779
Qy	744	MKESLTEVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKIS	803
Db	780	-----KKTPAKSTPAKTAVKKEASS	799
Qy	804	LQMEEFNNTAIYSNDDLSSKEDKIKESETFSOSSPIEIIDFPTFVSAKDDS--PKLAKE	861
Db	800	-----SSDDSSDDEKTKKKSATTPAKSTPKTALKKAESSDSSDDDEDLPKPSKA	848
Qy	862	YTDL-EVSDKSEIANIQSGADSLPCLEL-PCDLSFKNIYPKDEVHVSDEFSENRSSVSKA	919
Db	849	VTPRPQRADSEESAETEESSTRTALKAKPLATSTEKAVYENRRKRKSSPF--RRVQMTKD	906
Qy	920	SIS	922
Db	907	SVS	909

RESULT 15

QRMSP1

microtubule-associated protein MAP1B - mouse

N;Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protein MAP1.2; microtubule-associated protein MAP5

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 01-Sep-2000

C;Accession: S07549; S44387; A33645

R;Noble, M.; Lewis, S.A.; Cowan, N.J.

J. Cell Biol. 109, 3367-3376, 1989

A;Title: The microtubule binding domain of microtubule-associated protein MAP1B contains a repeated sequence motif unrelated to that of MAP2 and tau.

A;Reference number: A33645; MUID:90094539; PMID:2480963

A;Accession: S07549

A;Molecule type: mRNA

A;Residues: 1-2464 <NOB>

A;Cross-references: EMBL:X51396; NID:g52999; PIDN:CAA35761.1; PID:g53000

R;Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.

Arch. Biochem. Biophys. 310, 428-432, 1994

A;Title: Binding of heat-shock protein 70 (hsp70) to tubulin.

A;Reference number: S44387; MUID:94234720; PMID:8179328

A;Accession: S44387

A;Status: preliminary

A;Molecule type: protein

A;Residues: 653-663,'IC' <SAN>

C;Superfamily: microtubule-associated protein MAP1B

C;Keywords: microtubule binding; phosphoprotein; tandem repeat

F;589-786/Domain: microtubule binding #status experimental <MTB>

F;589-592,639-642,649-652,655-658,660-663,668-671,674-677,679-682,683-686,687-690,691-694,695-698,699-702,708-711,712-715,716-719,720-723,727-730,758-761,764-767,783-786/Region: 4-residue repeats (K/R-K-E/D-X)

F;1861-2064/Region: 17-residue repeats

F;91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: phosphate (Ser) (covalent) #status predicted
 F;147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (covalent) #status predicted
 F;1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 4.9%; Score 284; DB 1; Length 2464;
 Best Local Similarity 20.7%; Pred. No. 0.00093;
 Matches 233; Conservative 159; Mismatches 424; Indels 312; Gaps 51;

Qy	31	EPEDDEDEEEEEDEED-----DEDLEELE-----VLERKPAAG-----LSAAAVP	71
		: : : : :	
Db	1009	EAEQSEEEGEEEDKAEDAREEGYEPDKTEADYVMAVADKAAEAGVTEEQYGYLGTSKQ	1068
Qy	72	PAAAAPLLDFSS----DSVPPAPRGPLPAAPPAAPERQP-----SWERSPAAPA	116
		: : : : : : :	
Db	1069	PGIQSPSREPASSIHDETLPGGSESEATASDEENREDQPEEFTATSGYTQSTIEISSEPT	1128
Qy	117	P---SLPPAAAVLPSKLPEDDEPPARP-----PPPPPAGASPLAEP--	155
		: : : : : : : :	
Db	1129	PMDEMSTPRDVMSDETNNETESPSQEFVNITKYESSLYSQEYSKPAVASFENGLSEGSKT	1188
Qy	156	-----APPSTPAAPKRRGSGSVDETFLALPA-----ASEPVIPSSAEKIMDLMEQ	200
		: : : : : : :	
Db	1189	DATDGKDYNASASTISPP-----SSMEEDKFSKSALRDAYCSEEKELKASAE--LDIKDV	1241
Qy	201	PGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNLSAVSSSEGTTIEETLNEA	260
		:	
Db	1242	SDERLS-----PAKSPSLSP-----SPPSPIEKT----	1265
Qy	261	SKELPERATNPFVNRDLAEFS----ELEYSEMGSFSGSPKGESAILVEN--TKEEVIVR	314
		: : : : : :	
Db	1266	--PLGERSVN-----FSLTPNEIKVSAEGEARSVSPGVTQAVVEEHCASPEEKTLE	1314
Qy	315	SKDKEDLVCSAALHSP-QESPVGKEDRVVSPEKTMDFNEMQMSVVA-PVREEYADFK--	370
		: : : : : : : :	
Db	1315	VVSPSQSVTGSAGHTPPYQSP-----TDEKSSHLPTVESENAQAVPVSFSEAKDE	1366
Qy	371	-----PFEQAWEVKDTYEGSRDVLAAARANVESKVDKCLE--SLEQKSLGKDS----	417
		: : : : : : :	
Db	1367	NERASLSPMDE--PVPDSESPVEKVLSPLRSPPLLGSESPYEDFLSADSKVLGRRSESPF	1424
Qy	418	EGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLEDHTSENKT-----	470
		: : : : : :	
Db	1425	EGKNGKQGFPDRESPVSDLT----STGLYQDKQEEKSTGFIPIKEDFGPEKKTSDVETMS	1480
Qy	471	-----DEKKI-----EERKAQIITEKTSPKTSNPFLVAVQDSEAD	505
		: : : : : :	
Db	1481	SQSALALDERKLGGDVSPQTQIDVSQFGSFKEDTKMSISEGTVSDKSATPVDEGV--AEDT	1538
Qy	506	YVTTDTLSKVTEAAV--SNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAI	563
		: : : : : : : : : :	
Db	1539	YSHMEGVASVSTASVATSSFPPTDD--VSPSLHAEVGSHPHSTEVDDSLVSVVQTPPTTF	1597
Qy	564	QES-LYPTAQLCP---SFEEAEATP-----SPVLPDIVMEAPLNSLL--	601
		: : : : : : : : : :	
Db	1598	QETEMSPSKEECPRPMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSFAMD	1657

Qy 602 -----PSAGASVVQPSVSPLEAPPPVSYD-----SIKLEPENPPPPYEEAMNVA 644
 | : | | | : : : | | | | : | | : : :
 Db 1658 FSRQSPDHPTLGASVLHITEN---GPTEVDYSPCDIQDSSLSHKIPPTTEEPSYTQDNDLS 1714

Qy 645 LKALGTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDFSNYSEIAKFEKS 704
 : : : | : : | | | : : | : | : : |
 Db 1715 -ELISVSQVEASPSTSSAHTPS-----QIASPLQEDTLSDVVPREMSLYASLA----- 1762

Qy 705 VPEHAELVEDSSPESEPVDFSDDSIPEVPQTQEEAVML----MKESLTEVSETVAQHKE 760
 : | : | | : | | | | : | : | : | | |
 Db 1763 ----SEKVQ--SLEGEKLSPKSDIS----PLTPRESSPLYSPGFSDDSTSAAKETAAAH-- 1810

Qy 761 ERLSASP---QELGKPY-----LESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFN 810
 : | : | : | : : | : | : : : : | : : | : |
 Db 1811 -QASSSPPIDAATAEPYGFSSMLFDTMQHHLALNRDLTTSSV----EKDSGGKTPGDFN 1865

Qy 811 TAIYSNDDLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDSPK----LAKEYTDLE 866
 | : : | : : : | | | | : : : | : : | : |
 Db 1866 YAYQKPENAAGSPDEEDYDYE--SQEKTIRTHDVVRYYYEKTERTIKSPCDSGYSYETIE 1923

Qy 867 VSDKSEIANIQSGADSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRRSSVSKAS----- 920
 : | : : | | : : | : | | | : : | : : |
 Db 1924 KTTKTP----EDGG-----YTCEITEKTTRTPEEGGYSYEISEKTTRTPEVSGYTYEK 1972

Qy 921 -----ISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRS 962
 : : : : | : | : | : : | | | |
 Db 1973 TERSRRLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSFPESESYS 2020

Search completed: September 3, 2004, 16:09:46
 Job time : 37.8344 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 3, 2004, 16:09:02 ; Search time 114.801 Seconds
(without alignments)
3191.803 Million cell updates/sec

Title: US-09-830-972-2
Perfect score: 5848
Sequence: 1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRKAD 1163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 1298764

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description

1	5848	100.0	1163	9	US-09-893-348-18	Sequence 18, Appl
2	5307	90.7	1163	12	US-10-267-502-431	Sequence 431, App
3	4403.5	75.3	1192	9	US-09-758-140-6	Sequence 6, Appli
4	4403.5	75.3	1192	9	US-09-972-599A-6	Sequence 6, Appli
5	4403.5	75.3	1192	14	US-10-060-036-71	Sequence 71, Appl
6	4398.5	75.2	1192	9	US-09-789-386-2	Sequence 2, Appli
7	4398.5	75.2	1192	9	US-09-893-348-23	Sequence 23, Appl
8	4398.5	75.2	1192	12	US-10-267-502-429	Sequence 429, App
9	4398.5	75.2	1192	16	US-10-327-213-9	Sequence 9, Appli
10	4398.5	75.2	1192	16	US-10-466-258-9	Sequence 9, Appli
11	4389.5	75.1	1192	12	US-10-408-967-7	Sequence 7, Appli
12	1513	25.9	379	14	US-10-205-194-164	Sequence 164, App
13	1411.5	24.1	360	9	US-09-893-348-20	Sequence 20, Appl
14	1191	20.4	373	9	US-09-789-386-6	Sequence 6, Appli
15	1191	20.4	373	9	US-09-765-205-6	Sequence 6, Appli
16	1191	20.4	373	9	US-09-893-348-24	Sequence 24, Appl
17	1191	20.4	373	12	US-10-408-967-8	Sequence 8, Appli
18	1191	20.4	373	14	US-10-060-036-72	Sequence 72, Appl
19	1183	20.2	373	16	US-10-466-258-4	Sequence 4, Appli
20	925	15.8	199	9	US-09-893-348-21	Sequence 21, Appl
21	908	15.5	199	9	US-09-893-348-25	Sequence 25, Appl
22	908	15.5	199	12	US-10-660-946-1	Sequence 1, Appli
23	901	15.4	199	12	US-10-408-967-9	Sequence 9, Appli
24	899	15.4	199	12	US-09-978-360A-467	Sequence 467, App
25	888	15.2	289	9	US-09-789-386-4	Sequence 4, Appli
26	868	14.8	199	16	US-10-466-258-11	Sequence 11, Appl
27	801	13.7	777	14	US-10-205-219-93	Sequence 93, Appl
28	792	13.5	780	12	US-10-267-502-432	Sequence 432, App
29	789.5	13.5	776	12	US-10-660-946-5	Sequence 5, Appli
30	789.5	13.5	776	12	US-10-267-502-430	Sequence 430, App
31	716.5	12.3	356	12	US-10-660-946-6	Sequence 6, Appli
32	706.5	12.1	593	15	US-10-108-260A-2892	Sequence 2892, Ap
33	685	11.7	208	12	US-10-660-946-7	Sequence 7, Appli
34	671	11.5	267	12	US-10-660-946-8	Sequence 8, Appli
35	671	11.5	267	14	US-10-205-194-127	Sequence 127, App
36	630	10.8	266	12	US-10-276-774-2330	Sequence 2330, Ap
37	625.5	10.7	236	9	US-09-729-674-20	Sequence 20, Appl
38	625.5	10.7	236	9	US-09-765-205-26	Sequence 26, Appl
39	625.5	10.7	236	12	US-10-408-967-2	Sequence 2, Appli
40	625.5	10.7	269	14	US-10-106-698-6222	Sequence 6222, Ap
41	539.5	9.2	168	10	US-09-809-391-563	Sequence 563, App
42	539.5	9.2	168	10	US-09-882-171-563	Sequence 563, App
43	539.5	9.2	168	12	US-10-164-861-563	Sequence 563, App
44	520	8.9	222	12	US-10-267-502-428	Sequence 428, App
45	519	8.9	241	12	US-10-660-946-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-893-348-18

; Sequence 18, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.
 ; APPLICANT: BESERMAN, Pierre
 ; APPLICANT: MOSONEGO, Alon
 ; APPLICANT: MOALEM, Gila
 ; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
 THEIR USES
 ; FILE REFERENCE: EIS-SCHWARTZ=2A
 ; CURRENT APPLICATION NUMBER: US/09/893,348
 ; CURRENT FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US 09/314,161
 ; PRIOR FILING DATE: 1999-05-19
 ; PRIOR APPLICATION NUMBER: US 09/218,277
 ; PRIOR FILING DATE: 1998-12-22
 ; PRIOR APPLICATION NUMBER: PCT/US98/14715
 ; PRIOR FILING DATE: 1998-07-21
 ; PRIOR APPLICATION NUMBER: IL 124500
 ; PRIOR FILING DATE: 1998-05-19
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 1163
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-09-893-348-18

Query Match 100.0%; Score 5848; DB 9; Length 1163;
 Best Local Similarity 100.0%; Pred. No. 5.8e-287;
 Matches 1163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	181	AASEVPVPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL	240
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Db	241	GNLSAVSSSEGTTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSFFKGSPKGES	300
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Db	301	AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA	360
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Db	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Qy	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Db	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Qy	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Db	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Qy	1021	VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Db	1021	VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Qy	1081	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGIA	1140
Db	1081	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGIA	1140
Qy	1141	NKSVKDAMAKIQAKIPGLKRRKAD	1163
Db	1141	NKSVKDAMAKIQAKIPGLKRRKAD	1163

RESULT 2

→ US-10-267-502-431 ←
; Sequence 431, Application US/10267502
; Publication No. US20040071700A1

```
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 431
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-267-502-431
```

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Query Match          90.7%; Score 5307; DB 12; Length 1163;
Best Local Similarity 91.1%; Pred. No. 1.2e-259;
Matches 1066; Conservative 34; Mismatches 56; Indels 14; Gaps 7;
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Qy      1 MEDIDQSSLVSSSTDSPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEELEVLERK 60
          |||||
Db      1 MEDIDQSSLVSSSADSPRPPPAFKYQFVTEPEDEEDEEDEE-EEEDDEDLEELEVLERK 59

Qy     61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
          |||||
Db     60 PAAGLSAVPVPP-AAAPLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAASAPSLP 118

Qy    121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRGSGSVDETFLFALP 180
          |||||
Db    119 PAAAVLPSKLPEDDEPPAR--PPAPAGASPLAEPAAAPPSTPAAPKRRGSGSVDETFLFALP 176

Qy    181 AASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
          |||||
Db    177 AASEPVI PSSAEKIMDLKEQPGNTVSSGQEDFPSVLFTAASLPSLSPLSTVSFKEHGYL 236

Qy    241 GNLSAVSSSEG TIEETLNEASKELPERATNP FVNRDLAEFSELEYSEMGS SFGSPKGES 300
          |||||:|:|||||:|||||:|||||:|||||:|||||
Db    237 GNLSAVASTE G TIEETLNEASRELPERATNP FVNRESAEFSVLEYSEMGS SFGSPKGES 296

Qy    301 AILVENTKEEVIVRSKDKEDLVC SAALHSPQESP-----VGKEDRVVSPEKTMDIFNEMQ 355
          |:|||||:|||||:|||||:|||||:|||||:|||||
Db    297 AMLVENTKEEVIVRSKDKEDLVC SAALHNPQESPATLT KVVKEDGVMSPEKTMDIFNEMK 356

Qy    356 MSVVAPVREEYADFKPF EQAWEVKDTYEGSRDVLAA RANVESKVDRKCLED SLEQKSLGK 415
          |||||:|||||:|||||:|||||:|||||
Db    357 MSVVAPVREEYADFKPF EQAWEVKDTYEGSRDVLAA RANMESKVDDKKCFED SLEQKSHGK 416

Qy    416 DSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFP LLEDHTSENKTDEKKI 475
          ||| |||:||||| ||| ||||| ||||| ||| ||:|||||
Db    417 DSESRNENASFPSTPELVKDGSRAYITCDSFTSATESTANIFPV LEDHTSENKTDEKKI 476

Qy    476 EERKAQIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEA 535
          |||||:|||||:|||||:|||||:|||||:|||||
Db    477 EERKAQIITEKTS PKTSNPFLVAIH DSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA 536

Qy    536 CESELNEATG TKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEA 595
          |||||:|||||:|||||:|||||:|||||
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Db	537	CESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEA	596
Qy	596	PLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIK	655
Db	597	PLNSLLPSTGASVAQPSASPLEVSPVSYDGIKLEPENPPPYEEAMSVALKTSDAKEEIK	656
Qy	656	EPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDS	715
Db	657	EPESFNAAAQEAAPYISIIACDLIKETKLSTEPSPGFSNYSEIAKFEKSVPDHCELVDSDS	716
Qy	716	SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-EERLSASPQELGKPY	774
Db	717	SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVTQHKHKERLSASPQEVGKPY	776
Qy	775	LESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFS	834
Db	777	LESFQPNLHITKDAASNEIPTLTKEKETISLQMEEFNTAIYSNDDLSSKEDKMKESETFS	836
Qy	835	DSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSF	894
Db	837	DSSPIEIIDEFPTFVSAKDDSP---KEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSF	893
Qy	895	KNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPS	954
Db	894	KNTYPKDEAHVSDEFKSKRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKKLPS	953
Qy	955	DTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAY	1013
Db	954	DTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAY	1013
Qy	1014	IALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNST	1073
Db	1014	IALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNST	1073
Qy	1074	IKELRRLFLVDDLVDLSLKFAVLMWVFYVGALFNGLTLLILALISLFSIPVIYERHQVQI	1133
Db	1074	IKELRRLFLVDDLVDLSLKFAVLMWVFYVGALFNGLTLLILALISLFSIPVIYERHQAQI	1133
Qy	1134	DHYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	1134	DHYLGLANKSVKDAMAKIQAKIPGLKRKAE	1163

US-09-758-140-6

; Sequence 6, Application US/09758140

; GENERAL INFORMATION:

; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth

; CURRENT APPLICATION NUMBER: US/09/758,140

; PRIOR APPLICATION NUMBER: US 60/175,707

; PRIOR APPLICATION NUMBER: US 60/207,366

; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-140-6

Query Match 75.3%; Score 4403.5; DB 9; Length 1192;
Best Local Similarity 75.9%; Pred. No. 5.6e-214;
Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;

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Qy      1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDEDEDEDELEEVLERK 60
      |||:|||| ||||| ||||| ||||| ||||| |||||:||||:|||||
Db      1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDELEEVLERK 58

Qy     61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| || ||| |||: || :| ||||| ||||| ||||| ||| : |
Db     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSTVP 118

Qy    116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| |||| ||||| ||||| ||||| || || | ||||| |||||
Db    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178

Qy    167 RG-SGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
      || ||||| ||||| ||||| ||||| || |||||: ||: ||||| |||||
Db    179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy    226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
      ||||| ||||| ||||| | :|||: || :|||: ||: || :||| |||||
Db    238 LSPLSAAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy    286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
      ||||| || ||| |||: || | :||: ||: ||: || : || : || || ||
Db    298 SEMGSSFSVSPKAESAVIVANPREETIIVKNKDEEEKLVSNILHNQQELPTALTKLVKED 357

Qy    340 RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWEVKDTYEGSRDVLAA----RANV 395
      ||| || | ||| :|| ||: ||||| |||||: |||||: || | :||| :||:
Db    358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy    396 ESKVDRKCLEDLSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
      |||||: || ||||| : ||||| |: ||||| : || | ||||| | :|||
Db    417 ESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIA 476

Qy    455 ANTFFLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
      | |||| | ||||| |||||: ||||: || || ||||| |||| ||||| |:
Db    477 TNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536

Qy    514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
      |||| |: ||||| ||||| ||||| ||||| |||||: ||||| : ||||| |||
Db    537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL 596

Qy    574 CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYSIKLEPEN 633
      |||||: ||||| ||||| ||||| ||||| ||||| ||||| |: ||| ||||
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Db 597 CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN 655

Qy 634 PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDF 692
 |||||:|:| : | || |||||: |||:||||| ||||| ||:|

Db 656 PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDF 715

Qy 693 SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS 752
 |:|:|:| | : |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 716 SDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETS 775

Qy 753 -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF 809
 |: : : : |:| | | |||||: :| :| : : |:| | | |

Db 776 FESMIEYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEEL 835

Qy 810 NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVS 868
 :|:|:| | | |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 836 STAVYSNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSEFSKLAREYTDLEVS 895

Qy 869 DKSEIANIQSGADSLPCLSLPCDLSEFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV 926
 ||||| | | ||| | | ||| | : : |:|:| |:| :| :|

Db 896 HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPV 955

Qy 927 SALEPQTEMGSIKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986
 || | |: | | | | |||||: | |||||

Db 956 SALATQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK 1015

Qy 987 KTGTVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA 1046
 |||||

Db 1016 KTGTVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA 1075

Qy 1047 YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLKFVLMWVFTYVGALF 1106
 |||||

Db 1076 YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKFVLMWVFTYVGALF 1135

Qy 1107 NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRRKAD 1163
 |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 1136 NGLTLLILALISLFSVPVIYERHQVQIDHYLGLANKNVKDAMAKIQAKIPGLKRRKAE 1192

RESULT 4

US-09-972-599A-6

; Sequence 6, Application US/09972599A

; Patent No. US20020077295A1

; GENERAL INFORMATION:

; APPLICANT: STRITTMATTER, STEPHEN M.

; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH

; FILE REFERENCE: C077 CIP US

; CURRENT APPLICATION NUMBER: US/09/972,599A

; CURRENT FILING DATE: 2001-10-06

; PRIOR APPLICATION NUMBER: PCT/US01/01041

; PRIOR FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 09/758,140

; PRIOR FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 60/236,378

; PRIOR FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: 60/207,366

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/175,707
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-599A-6

Query Match 75.3%; Score 4403.5; DB 9; Length 1192;
Best Local Similarity 75.9%; Pred. No. 5.6e-214;
Matches 909; Conservative 104; Mismatches 145; Indels 39; Gaps 20;

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Qy      1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEELEVLERK 60
      |||:|||| ||||| ||||| ||||| ||||| |||||:|::| ||||| |||||
Db      1 MEDLDQSPLVSSS-DSPRRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEELEVLERK 58

Qy     61 PAAGLSAAAVP--PAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| || |||:| | : ||||| ||||| |||||: || : |
Db     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSSTVP 118

Qy    116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| |||| ||||| ||||| ||||| || || ||||| |||||
Db    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178

Qy    167 RG-SGSVDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
      || ||||| ||||| ||||| |||| ||| |||||:|:| ||||| |||||
Db    179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy    226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
      ||||| ||||| ||||| | :|||:| :|||:| :| :||| |||||
Db    238 LSPLSAAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy    286 SEMGSSFKGSPKGESAILVENTKKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
      ||||| || |||:| | :||:|:|:|:|: || : ||: || |||
Db    298 SEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKED 357

Qy    340 RVVSPEKTMDFNEMQMSVVPVREEYADFKPFQAWEVKDTYEGSRDVLAA----RANV 395
      ||| || | ||| :|| | ||:|||||||: ||||: | | |:||| :|:
Db    358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy    396 ESKVDRKCLEDSELEQSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
      |||||:| ||||| : ||||| |:| ||||| :|| | ||||| | :|||
Db    417 ESKVDKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIA 476

Qy    455 ANTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
      | |||| | ||||| |||||:||||:| || ||||| ||||| ||||| |:
Db    477 TNIFPLLGDPSTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNL 536

Qy    514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
      |||| |:||||| ||||| ||||| |||||:||||| :|||| |||
Db    537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL 596

Qy    574 CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN 633
      |||||:||||| ||||| :|||||:| ||||| |:| ||| |||
Db    597 CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN 655
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Qy	634	PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQTEAPYISIACDLIKETKLSTEPSPDF	692
Db	656	PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQTEAPYISIACDLIKETKLSAEPAPDF	715
Qy	693	SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS	752
Db	716	SDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDPVQKQDETVMVLKESLTETS	775
Qy	753	-ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF	809
Db	776	FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEEL	835
Qy	810	NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIIDEFPTFVSAKDDS-PKLAKEYTDLEVS	868
Db	836	STAVYSNDDLFIKESKAEQIRETETFSFSDSSPIEIIIDEFPTLISSKTDSEFSLAREYTDLEVS	895
Qy	869	DKSEIANIQSGADSLPCLLELPDCLSFKNYIPK--DEVHVSDEFSENRSSVSKASISPSNV	926
Db	896	HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDV	955
Qy	927	SALEPQTEMGSIKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK	986
Db	956	SALATQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK	1015
Qy	987	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1046
Db	1016	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1075
Qy	1047	YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1106
Db	1076	YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1135
Qy	1107	NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	1136	NGLTLLILALISLFSVPVIYERHQVQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 5

US-10-060-036-71

; Sequence 71, Application US/10060036

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; Publication No. US20030073144A1
```

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

; APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yuqiu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

; FILE REFERENCE: 210121.566

; CURRENT APPLICATION NUMBER: US/10/060,036

: CURRENT FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 4560

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; SOFTWARE: FastSEQ for Windows Version 4.0
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; SEQ ID NO 71

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; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-71
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Qy	1	MEDIDQSSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEEDDEEEEDDEEDLEELEVLERK	60
Db	1	MEDLDQSPLVSSS--DSPRRPQPAFKYQFVREPEDEE-EEEEEEEDDEDEDLEELEVLERK	58
Qy	61	PAAGLSAAAVP--PAAAAPLLDFSSDSVPAPRGLPAAPPAAPERQPSWERSPAA---P	115
Db	59	PAAGLSAAPVPTAPAAGAPLMDFGNDVFPPAPRGLPAAPPVAPERQPSWDPSPVSSSTVP	118
Qy	116	APSLPPAAAVLP SKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Db	119	APSPLSAAAVSP SKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR	178
Qy	167	RG-SGSVDETFLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS	225
Db	179	RGSSGSVDETFLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS	237
Qy	226	LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY	285
Db	238	LSPLSAA SFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY	297
Qy	286	SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED	339
Db	298	SEMGSSFVSVPKAE SAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALT KLVKED	357
Qy	340	RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAW EVKDTYEGSRDVLAA----RANV	395
Db	358	EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL	416
Qy	396	ESKVDRCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT	454
Db	417	ESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIA	476
Qy	455	ANTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS	513
Db	477	TNIFPLLGDP TSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT	536
Qy	514	KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL	573
Db	537	KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL	596
Qy	574	CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYSIKLEPEN	633
Db	597	CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN	655
Qy	634	PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDF	692
Db	656	PPPYEEAMSVSLKKVSGIKEEIKEPENINAALOETEAPYISIIACDLIKETKLSAEPAPDF	715

Query Match 75.2%; Score 4398.5; DB 9; Length 1192;
Best Local Similarity 75.9%; Pred. No. 1e-213;
Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

Qy	1	MEDIDQSSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEDEEEDDEELEELEVLERK	60
Db	1	MEDLDQSPLVSSS-DSPRRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK	58
Qy	61	PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P	115
Db	59	PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSPVSTVP	118
Qy	116	APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Db	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR	178
Qy	167	RG-SGSVDETTLFALPAASEPVIPISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS	225
Db	179	RGSSGSVDETTLFALPAASEPVISSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS	237
Qy	226	LSPLSTVSVFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY	285
Db	238	LSPLSAAAFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLIDRDLTEFSELEY	297
Qy	286	SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED	339
Db	298	SEMGSSFVSVPKSAESAVIVANPREEIIIVKNKDEEEKLVSNNIHNNQQLPTALTCLKVKED	357
Qy	340	RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWEVKDTYEGSRDVLAA----RANV	395
Db	358	EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL	416
Qy	396	ESKVDRCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT	454
Db	417	ESKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIA	476
Qy	455	ANTFPLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS	513
Db	477	TNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT	536
Qy	514	KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL	573
Db	537	KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL	596
Qy	574	CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLAAPPVSYDSIKLEPEN	633
Db	597	CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN	655
Qy	634	PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDF	692
Db	656	PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDF	715
Qy	693	SNYSEIAKFEKSVPEHAELVEDSSPESEPVDFSDDSIPEVPQTQEEAVMLMKESLTEVS	752
Db	716	SDYSEMAKVEQVPDPHSELVEDSSPDSEPVDFSDDSIPDPVPOKODETVMVVKESLTETS	775

Qy	753	-ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF	809
Db	776	FESMIEYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEEL	835
Qy	810	NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDFPTFVSAKDDS-PKLAKEYTDLEVS	868
Db	836	STAVYSNDDLFIKSAQIRETETFSDDSSPIEIIDFPTLISSTKTSDFSKLAREYTDLEVS	895
Qy	869	DKSEIANIQSGADSLPCLLPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV	926
Db	896	HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDV	955
Qy	927	SALEPQTEMGSIVKSKSLTKEAEKKLPSPDTEKEDRSLSAVISAELSKTSVVDLLYWRDIK	986
Db	956	SALATQAEIESIVKPKVLVKEAEKKLPSPDTEKEDRSPSAISAELSKTSVVDLLYWRDIK	1015
Qy	987	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1046
Db	1016	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1075
Qy	1047	YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1106
Db	1076	YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1135
Qy	1107	NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	1136	NGLTLLILALISLFSVPVIYERHQAOIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

US-09-893-348-23

; Sequence 23, Application US/09893348

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500

; PRIOR FILING DATE: 1998-05-19

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; NUMBER OF SEQ ID NOS: 29
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; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 23

; LENGTH: 1192

; ORGANISM: Homo sapiens
US-09-893-348-23

Query Match 75.2%; Score 4398.5; DB 9; Length 1192;
Best Local Similarity 75.9%; Pred. No. 1e-213;
Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

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Qy      1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
      |||:|||| ||||| ||||| ||||| ||||| |||||:|:|:|||||
Db      1 MEDLDQSPLVSSS-DSPRPQPAFKYQFVREPEDEE-EEEEEEDEDEDLEEEVLERK 58

Qy     61 PAAGLSAAAVP--PAAAAPLLDFSSDVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| || ||| |||:| | :| ||||| ||||| |||||: || : |
Db     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDFSPVSSTVP 118

Qy    116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178

Qy    167 RG-SGSVDETLFALPAASEPVI PSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
      || ||||| ||||| ||||| ||||| ||||| |||||:|:| ||||| |||||
Db    179 RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy    226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY 285
      ||||| ||||| ||||| | :|||:| :|||:| :| :||| |||||
Db    238 LSPLSAAAFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy    286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
      ||||| ||| |||:| | :|||:|:|:|:| | : ||: || | |||
Db    298 SEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKED 357

Qy    340 RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWVKDITYEGSRDVLAA----RANV 395
      ||| || | ||| :|:| ||:||||| |||: |||: | | |:||| :|:
Db    358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy    396 ESKVDRKCLEDLSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
      |||||:| |||| : |||| |:| ||||| :|| ||||| | :|||
Db    417 ESKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIA 476

Qy    455 ANTFLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
      | |||| | ||||| |||||:|||:| || ||||| |||| ||||| |:
Db    477 TNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536

Qy    514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
      |||| |:||||| ||||| ||||| |||||:||||| :||||| |||
Db    537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL 596

Qy    574 CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN 633
      |||||:||||| ||||| :|||||:||| |||| |:|:| |||
Db    597 CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN 655

Qy    634 PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDF 692
      |||||:|:| | : | || ||||: |||:||||| ||||| ||:|
Db    656 PPPYEEAMSVSLKKVSGIKEEIKPENINAALQETEAPYISACDLIKETKLSAEPAPDF 715

Qy    693 SNYSEIAKFESVPEHAELVEDSSPESEPVDFLSDDSIPEVPQTQEEAVMLMKESLTEVS 752
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Qy 61 PAAGLSAAAVP--PAAAAPLLDFFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
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Db 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVP 118

Qy 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
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Db 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178

Qy 167 RG-SGSVDETLFALPAASEFVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS 225
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Db 179 RGSSGSVDETLFALPAASEFVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS 237

Qy 226 LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLINEASKELPERATNPFVNRDLAEFSELEY 285
 ||||| ||||| ||||| | :|||:| :|||:| :| :||| |||||

Db 238 LSPLSAAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY 297

Qy 286 SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED 339
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Db 298 SEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQLPTALTCLVKED 357

Qy 340 RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWEVKDTYEGSRDVLAA----RANV 395
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Db 358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy 396 ESKVDRKCLEDSELEQSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
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Db 417 ESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIA 476

Qy 455 ANTFPILLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
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Db 477 TNIFPLLGDPTSSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536

Qy 514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
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Db 537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTGIAYETKMDLVQTSEVMQESLYPAAQL 596

Qy 574 CPSFEEAEATPSVLPDIMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN 633
 |||||:||||| ||||| :|||||:||| |||| |:|:||| ||||

Db 597 CPSFEESEATPSVLPDIMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN 655

Qy 634 PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDF 692
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Db 656 PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDF 715

Qy 693 SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS 752
 |:|:|:| |: |:|:|:|||||:||||| ||| |:| |:|:|:| |

Db 716 SDYSEMAKVEQVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLESILTETS 775

Qy 753 -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF 809
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Db 776 FESMIEYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEEL 835

Qy 810 NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIIDEFPTFVSAKDDS-PKLAKEYTDLEVS 868
 |:|:|:| ||| |:|:|:||||| ||||| :|:| || |:|:|:|

Db 836 STAVYSNDDLFIKSEAQIRETETFSDDSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVS 895

Qy	869	DKSEIANIQSGADSLPCLLELPCLDSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV	926
Db	896	HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDV	955
Qy	927	SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK	986
Db	956	SALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK	1015
Qy	987	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1046
Db	1016	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1075
Qy	1047	YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1106
Db	1076	YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1135
Qy	1107	NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	1136	NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

Query Match 75.2%; Score 4398.5; DB 16; Length 1192;
Best Local Similarity 75.9%; Pred. No. 1e-213;
Matches 908; Conservative 104; Mismatches 146; Indels 39; Gaps 20;

Qy	167	RG-SGSVDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS	225
Db	179	RGSSGSVDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS	237
Qy	226	LSPLSTVSVFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY	285
Db	238	LSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY	297
Qy	286	SEMGSSFKGSPKGESAILVENTKKEEVIVRSKDKED-LVCSAALHSPQESVPG-----KED	339
Db	298	SEMGSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKED	357
Qy	340	RVVSPEKTMDIFNEMQMSVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANV	395
Db	358	EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL	416
Qy	396	ESKVDKRCLEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDDSSRAYITCASFT-SATESTT	454
Db	417	ESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIA	476
Qy	455	ANTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFVLVAVQDSEADYVTTDTLS	513
Db	477	TNIFPLLGDPSTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVLVAAQDSETDYVTTDNLT	536
Qy	514	KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL	573
Db	537	KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL	596
Qy	574	CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPEN	633
Db	597	CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPEN	655
Qy	634	PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDF	692
Db	656	PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDF	715
Qy	693	SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS	752
Db	716	SDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPEVPQKQDETVMVLKESLTETS	775
Qy	753	-ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF	809
Db	776	FESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEEL	835
Qy	810	NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIIDEFPTFVSAKDDS-PKLAKEYTDLEVS	868
Db	836	STAVYSNDDLFIKESQAQIRETETFSDDSSPIEIIIDEFPTLISSKTDSSFKLAREYTDLEVS	895
Qy	869	DKSEIANIQSGADSLPCLELPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV	926
Db	896	HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPV	955
Qy	927	SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK	986
Db	956	SALATOAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK	1015

Db 298 SEMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKED 357

Qy 340 RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWEVKDTYEGSRDLAA----RANV 395
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Db 358 EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL 416

Qy 396 ESKVDRKCLEDSEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT 454
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Db 417 ESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIA 476

Qy 455 ANTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS 513
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Db 477 TNIFPLLGDPTSENKTDEKKIEEKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT 536

Qy 514 KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL 573
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Db 537 KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL 596

Qy 574 CPSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYSIKLEPEN 633
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Db 597 CPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSSPLEA-SSVNYESIKHEPEN 655

Qy 634 PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDF 692
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Db 656 PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDF 715

Qy 693 SNYSEIAKFEKSVPEHAELVEDSSPESEPVDFSDDSIPEVPQTQEEAVMLMKESLTEVS 752
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Db 716 SDYSEMAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETS 775

Qy 753 -ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF 809
 |: : : |:| | | |||||: :| :| | : : |:| |||| |

Db 776 FESMIEYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEEL 835

Qy 810 NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVS 868
 :|:|:| ||| |:|:|:|||||||:|:| | | |:|:| ||||

Db 836 STAVYSNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVS 895

Qy 869 DKSEIANIQSGADSLPCLELPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV 926
 |||| | | ||| ||| ||| ||| ||| : : |:|:| |: | :|:|

Db 896 HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDPV 955

Qy 927 SALEPQTEMGSIKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 986
 || | |: ||| | | |||||:|: | |||||

Db 956 SALATQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK 1015

Qy 987 KTGUVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA 1046
 |||||

Db 1016 KTGUVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA 1075

Qy 1047 YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF 1106
 |||||

Db 1076 YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF 1135

Qy 1107 NGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
 |||||:||||| |||||:|||||

Db 1136 NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 11
 US-10-408-967-7
 ; Sequence 7, Application US/10408967
 ; Publication No. US20040063161A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pharmacia & Upjohn Company
 ; APPLICANT: Yan, Riqiang
 ; APPLICANT: Lu, Yifeng
 ; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease
 ; FILE REFERENCE: 00925
 ; CURRENT APPLICATION NUMBER: US/10/408,967
 ; CURRENT FILING DATE: 2003-04-08
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 1192
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-967-7

Query Match 75.1%; Score 4389.5; DB 12; Length 1192;
 Best Local Similarity 75.8%; Pred. No. 2.9e-213;
 Matches 907; Conservative 104; Mismatches 147; Indels 39; Gaps 20;

Qy	1	MEDIDQSSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK	60
		:	
Db	1	MEDLDQSPLVSSS-DSPRRQPAFKYQFVREPEDEE-EDEEEEEDEDEDLEEEVLERK	58
Qy	61	PAAGLSAAAVP--PAAAPLLDFFSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P	115
Db	59	PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSSTVP	118
Qy	116	APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Db	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKR	178
Qy	167	RG-SGSVDETLFALPAASEVPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS	225
Db	179	RGSSGSVDETLFALPAASEPVIRSSAEN-MDLKEQPGNTISAGQEDFPSVLLETAASLPS	237
Qy	226	LSPLSTVSFKEHGYLGNL SAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY	285
Db	238	LSPLSAAASFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY	297
Qy	286	SEMGSFFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED	339
Db	298	SEMGSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKED	357
Qy	340	RVVSPEKTMDFNEMQMSVVAPVREEYADFKPFQAWVEVKDITYEGSRDVLAA----RANV	395
Db	358	EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL	416
Qy	396	ESKVDKCLDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTT	454
Db	417	ESKVDKKCFADSLEQTNHEKDESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIA	476


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; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018201
; CURRENT APPLICATION NUMBER: US/10/205,194
; CURRENT FILING DATE: 5200-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Foocen-m2 reticulon
US-10-205-194-164
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Query Match          25.9%; Score 1513; DB 14; Length 379;
Best Local Similarity 32.6%; Pred. No. 1.3e-68;
Matches 379; Conservative 0; Mismatches 0; Indels 784; Gaps 1;
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Qy      1 MEDIDQSSLVSSSTDSPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
          |||
Db      1 MEDIDQSSLVSSSTDSPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60

Qy      61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
          |||
Db      61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

Qy      121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRGSGSVDETFLFALP 180
          |||
Db      121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAAPPSTPAAPKRRGSGSVDETFLFALP 180

Qy      181 AASEPVIPSSAEKIMDLMEQP GNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
          |||
Db      181 AASEPVIPSSA----- 191

Qy      241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRLAEFSELEYSEMGSSEFKGSPKGES 300
Db      192 ----- 191

Qy      301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360
Db      192 ----- 191

Qy      361 PVREEYADFKPFQAWQEVKDTYEGSRDVLAAARANVESKVDRKCLEDSELEQKSLGKDSEGR 420
Db      192 ----- 191

Qy      421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTANTFPILLEDHTSENKTDEKKIEERKA 480
Db      192 ----- 191

Qy      481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540
```

Db	192	-----	191
Qy	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Db	192	-----	191
Qy	601	LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Db	192	-----	191
Qy	661	NAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	192	-----	191
Qy	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	192	-----	191
Qy	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	192	-----	191
Qy	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	192	-----	191
Qy	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Db	192	-----	191
Qy	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Db	192	-----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	236
Qy	1021	VTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Db	237	VTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	296
Qy	1081	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	1140
Db	297	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	356
Qy	1141	NKSVKDAMAKIQAKIPGLKRRAD	1163
Db	357	NKSVKDAMAKIQAKIPGLKRRAD	379

RESULT 13

US-09-893-348-20

; Sequence 20, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

```
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-893-348-20
```

```
Query Match          24.1%; Score 1411.5; DB 9; Length 360;
Best Local Similarity 31.0%; Pred. No. 1.7e-63;
Matches 360; Conservative 0; Mismatches 0; Indels 803; Gaps 1;
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Qy      1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK 60

Qy     61 PAAGLSAAAVPPAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PAAGLSAAAVPPAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

Qy    121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETLEFALP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSV----- 172

Qy    181 AASEPVIPISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
Db    173 ----- 172

Qy    241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSFSGSPKGES 300
Db    173 ----- 172

Qy    301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360
Db    173 ----- 172

Qy    361 PVREEYADFKPFQAWKDYEGSRDVLAAARANVESKVDRKCLEDSELEQKSLGKDSEGR 420
Db    173 ----- 172

Qy    421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLEDHTSENKTDEKKIEERKA 480
Db    173 ----- 172
```

Qy	481	QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Db	173	-----	172
Qy	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Db	173	-----	172
Qy	601	LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Db	173	-----	172
Qy	661	NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	173	-----	172
Qy	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	173	-----	172
Qy	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	173	-----	172
Qy	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSEFKNIYPK	900
Db	173	-----	172
Qy	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPDTEKED	960
Db	173	-----	172
Qy	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	1020
Db	173	-----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	217
Qy	1021	VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	1080
Db	218	VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	277
Qy	1081	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	1140
Db	278	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA	337
Qy	1141	NKSVKDAMAKIQAKIPGLKRKAD	1163
Db	338	NKSVKDAMAKIQAKIPGLKRKAD	360

RESULT 14

US-09-789-386-6

; Sequence 6, Application US/09789386

; Patent No. US20020010324A1

; GENERAL INFORMATION:

; APPLICANT: MICHALOVICH, DAVID

; APPLICANT: PRINJHA, RABINDER KUMAR

; TITLE OF INVENTION: NOVEL COMPOUNDS

```
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-6
```

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Query Match          20.4%; Score 1191; DB 9; Length 373;
Best Local Similarity 27.8%; Pred. No. 2.4e-52;
Matches 327; Conservative 12; Mismatches 20; Indels 818; Gaps 7;
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Qy      1 MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
      |||:|||| ||||| ||||| ||||| ||||| |||||:|::| ||||| |||||
Db      1 MEDLDQSPLVSSS-DSPRRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 58

Qy      61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| || ||| |||:| :| ||||| ||||| |||||: || : |
Db      59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVP 118

Qy      116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPAPAPAAPSTPAAPKR 178

Qy      167 RGSGSVDETLEFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226
      |||
Db      179 RGSS----- 182

Qy      227 SPLSTVSFKEHGYLGNLSAVSSSEGTTIEETLNEASKELPERATNPFVNRDLAEFSELEYS 286
Db      183 ----- 182

Qy      287 EMGSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESVPGKEDRVVSPEK 346
Db      183 ----- 182

Qy      347 TMDIFNEMQMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLED 406
Db      183 ----- 182

Qy      407 SLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTS 466
Db      183 ----- 182

Qy      467 ENKTDEKKIEERKAQIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEG 526
Db      183 ----- 182
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Qy	527	LTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSP	586
Db	183	-----	182
Qy	587	VLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALK	646
Db	183	-----	182
Qy	647	ALGTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDFSNYSEIAKFEKSVP	706
Db	183	-----	182
Qy	707	EHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSAS	766
Db	183	-----	182
Qy	767	PQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDK	826
Db	183	-----	182
Qy	827	IKESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCL	886
Db	183	-----	182
Qy	887	ELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTK	946
Db	183	----- :GSV-----	185
Qy	947	EAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS	1006
Db	186	----- VVDLLYWRDIKKTGVVFGASLFLLLSLTVFS	216
Qy	1007	IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA	1066
Db	217	----- IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA	276
Qy	1067	LGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIY	1126
Db	277	----- LGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIY	336
Qy	1127	ERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	337	----- ERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	373

RESULT 15

US-09-765-205-6

; Sequence 6, Application US/09765205

; Patent No. US20020034800A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Li

; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES

; FILE REFERENCE: 1458.004/200130.449

; CURRENT APPLICATION NUMBER: US/09/765,205

; CURRENT FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: US/09/212,440

; PRIOR FILING DATE: 1998-12-16


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; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: human
US-09-765-205-6
```

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Query Match          20.4%; Score 1191; DB 9; Length 373;
Best Local Similarity 27.8%; Pred. No. 2.4e-52;
Matches 327; Conservative 12; Mismatches 20; Indels 818; Gaps 7;
```

```
Qy      1 MEDIDQSSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
      |||:|||| ||||| ||||| ||||| ||||| |||||:|:|:|||||
Db      1 MEDLDQSPLVSSS-DSPRRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEEEVLERK 58

Qy     61 PAAGLSAAAVP---PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P 115
      ||||| || || ||| |||:| | :| ||||| ||||| |||||: || : |
Db     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVP 118

Qy    116 APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166
      ||| |||| ||||| ||||| ||||| || || || ||||| |||||
Db    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178

Qy    167 RGSGSVDETLFALPAASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL 226
      |||
Db    179 RGSS----- 182

Qy    227 SPLSTVSFKEHGYLGNSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS 286
Db    183 ----- 182

Qy    287 EMGSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEK 346
Db    183 ----- 182

Qy    347 TMDIFNEMQMSVVAPVREEYADFKPFQAWEVKDTYEGSRDVLAAARANVESKVDRKCLED 406
Db    183 ----- 182

Qy    407 SLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTS 466
Db    183 ----- 182

Qy    467 ENKTDEKKIEERKAQIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEG 526
Db    183 ----- 182

Qy    527 LTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSP 586
Db    183 ----- 182

Qy    587 VLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVALK 646
Db    183 ----- 182

Qy    647 ALGTKEGIKEPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVP 706
```

Db	183	-----	182
Qy	707	EHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSAS	766
Db	183	-----	182
Qy	767	PQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDK	826
Db	183	-----	182
Qy	827	IKESETFSDSSPIELIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCL	886
Db	183	-----	182
Qy	887	ELPCDLSEFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTK	946
Db	183	----- :-----GSV-----	185
Qy	947	EAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFS	1006
Db	186	----- -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFS	216
Qy	1007	IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA	1066
Db	217	IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA	276
Qy	1067	LGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVVGALFNGLTLLILALISLFSIPVIY	1126
Db	277	LGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVVGALFNGLTLLILALISLFSVPVIY	336
Qy	1127	ERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD	1163
Db	337	ERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	373

Search completed: September 3, 2004, 16:30:01
Job time : 122.801 secs

OM protein - protein search, using sw model

Run on: September 3, 2004, 15:59:39 ; Search time 73.0975 Seconds
(without alignments)
5019.975 Million cell updates/sec

Title: US-09-830-972-2
Perfect score: 5848
Sequence: 1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRRKAD 1163

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	5312.5	90.8	1162	11	Q8BGM9	Q8bgm9 mus musculu
2	5307	90.7	1163	11	Q8K3G8	Q8k3g8 mus musculu
3	4501.5	77.0	1046	11	Q8BGK7	Q8bgk7 mus musculu
4	3627.5	62.0	986	4	Q8IUA4	Q8iua4 homo sapien
5	3299.5	56.4	720	11	Q7TNB7	Q7tnb7 mus musculu
6	2926	50.0	639	11	Q8K290	Q8k290 mus musculu
7	2610	44.6	578	11	Q80W95	Q80w95 mus musculu
8	1416	24.2	375	11	Q8BHF5	Q8bhf5 mus musculu
9	1314.5	22.5	356	11	Q8BH78	Q8bh78 mus musculu
10	1304	22.3	357	11	Q8K3G7	Q8k3g7 mus musculu
11	1283.5	21.9	392	4	Q96B16	Q96b16 homo sapien
12	878	15.0	184	6	Q7YRW9	Q7yrw9 bos taurus
13	876	15.0	199	13	Q7T224	Q7t224 gallus gall
14	844	14.4	179	6	Q9GM33	Q9gm33 macaca fasc
15	792	13.5	780	11	Q8K4S4	Q8k4s4 mus musculu
16	788	13.5	780	11	Q8K0T0	Q8k0t0 mus musculu
17	762.5	13.0	760	13	Q90638	Q90638 gallus gall
18	737	12.6	214	13	Q7T222	Q7t222 carassius a
19	700	12.0	643	11	Q8CCU2	Q8ccu2 mus musculu
20	685	11.7	199	4	Q9BQ59	Q9bq59 homo sapien
21	671	11.5	267	11	Q63765	Q63765 rattus sp.
22	669	11.4	208	13	Q90637	Q90637 gallus gall
23	625.5	10.7	236	11	Q8VBU0	Q8vbu0 rattus norv
24	625.5	10.7	237	11	Q8C6D5	Q8c6d5 mus musculu
25	590.5	10.1	221	13	Q7ZUD6	Q7zud6 brachydanio
26	586	10.0	595	5	Q9VMV9	Q9vmv9 drosophila
27	532	9.1	224	5	Q9VMW1	Q9vmw1 drosophila
28	520	8.9	202	5	Q9VMW2	Q9vmw2 drosophila
29	520	8.9	222	5	Q9VMW4	Q9vmw4 drosophila
30	520	8.9	234	5	Q9VMW3	Q9vmw3 drosophila
31	517	8.8	2484	5	Q9U347	Q9u347 caenorhabdi
32	503.5	8.6	2607	5	Q23187	Q23187 caenorhabdi
33	377	6.4	2768	5	Q9VC00	Q9vc00 drosophila
34	347.5	5.9	10578	5	Q8ISF5	Q8isf5 caenorhabdi
35	344	5.9	107	13	Q7T223	Q7t223 carassius a
36	343.5	5.9	18519	5	Q8ISF6	Q8isf6 caenorhabdi
37	343.5	5.9	18534	5	Q8ISF7	Q8isf7 caenorhabdi
38	342.5	5.9	1417	3	Q871Y7	Q871y7 neurospora
39	335	5.7	5412	5	Q9W596	Q9w596 drosophila
40	331	5.7	4900	5	Q9N541	Q9n541 caenorhabdi
41	328.5	5.6	5327	5	O76891	O76891 drosophila
42	322	5.5	7962	4	Q10465	Q10465 homo sapien
43	320	5.5	222	5	Q23188	Q23188 caenorhabdi
44	317.5	5.4	17352	5	Q95YM2	Q95ym2 procambarus
45	313.5	5.4	1444	5	Q9VTN2	Q9vtn2 drosophila

ALIGNMENTS

RESULT 1

Q8BGM9

ID Q8BGM9 PRELIMINARY; PRT; 1162 AA.

AC Q8BGM9;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Qy 241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMSSFKGSPKGES 300
 |||||:|:|||||||:|||||||:||||| ||||| |||||

Db 237 GNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSEMSSFNKGSPKGES 296

Qy 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESP-----VGKEDRVVSPEKTMDFNEMQ 355
 |:|||||||:|||||||:||||| | ||| |:|||||||:

Db 297 AMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLTQVVKEDGVMSPEKTMDFNEMK 356

Qy 356 MSVVAPVREEYADFKPFQAWEVKDTYEGSRDVLAAARANVESKVDKCLEDSLEQKSLGK 415
 |||||:|||||:| ||||| ||

Db 357 MSVVAPVREEYADFKPFQAWEVKDTYEGSRDVLAAARANMESKVDKKCFEDSLEQKGHGK 416

Qy 416 DSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPILLEDHTSENKTDEKKI 475
 ||| |||:|||| ||| ||| ||||| |:||||| || |:|||||||

Db 417 DSESRNENASFPRTPELVKDGSRAYITCDSFSSATESTAANIFPVLEDHTSENKTDEKKI 476

Qy 476 EERKAQIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEA 535
 |||||:||||| ||||| |: |||||

Db 477 EERKAQIITEKTSPKTSNPFLVAIHQDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA 536

Qy 536 CESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSVLPDIVMEA 595
 |||||:||||| |||||

Db 537 CESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSVLPDIVMEA 596

Qy 596 PLNSLLPSAGASVVQPSVSPLAPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIK 655
 ||||| |||| ||| |||| | |||| |||||:|||| :|| ||

Db 597 PLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPPPYEEAMSVALKTSKSDSKEEIK 656

Qy 656 EPESFNAAVQETEAPYISACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDS 715
 ||||| || |||||:|||||:|||||:| |||:|

Db 657 EPESFNAQAQAEAPYISACDLIKETKLSTEPSPEFSNYSEIAKFEKSVPDHCELVDSDS 716

Qy 716 SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-EERLSASPQELGKPY 774
 |||||:||||| ||||| ||| :|||||:||||

Db 717 SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVTQHKHKERLSASPQEVGKPY 776

Qy 775 LESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFS 834
 ||||| |||||:||||| |||||:|||||

Db 777 LESFQPNLHITKDAASNEIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKMKESSETFS 836

Qy 835 DSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSF 894
 ||||| |||||:|||||:|||||:|||| |||||

Db 837 DSSPIEIIDEFPTFVSAKDDSP---KEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSF 893

Qy 895 KNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPS 954
 || |||| |||||:||||| : ||||| | |||:||| | |||||:||||

Db 894 KNTYPKDEAHVSDEFKSRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKKLPS 953

Qy 955 DTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYI 1014
 |||||:|||||:||||| |||||

Db 954 DTEKEDRSLTAVLSAELNKTTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYI 1013

Qy 1015 ALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTI 1074
 |||||

Db 1014 ALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTI 1073

```
QY      1075 KELRRFLVDDLVDLSLKFAVLMWVFYVGALFNGLTLLILALISLFSIPVIYERHQVQID 1134
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1074 KELRRFLVDDLVDLSLKFAVLMWVFYVGALFNGLTLLILALISLFSIPVIYERHQAQID 1133

QY      1135 HYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
        |||||||||||||||||||||||||:
Db      1134 HYLGLANKSVKDAMAKIQAKIPGLKRKAE 1162
```

RESULT 2

Q8K3G8

```

ID      Q8K3G8                PRELIMINARY;          PRT;  1163 AA.
AC      Q8K3G8;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Nogo-A.
GN      RTN4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c;
RA      Jin W., Long M., Li R., Ju G.;
RT      "Cloning and expression of the mouse Nogo-A protein.";
RL      Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AY114152; AAM77068.1; -.
DR      MGD; MGI:1915835; Rtn4.
DR      GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR      GO; GO:0007399; P:neurogenesis; IDA.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
SQ      SEQUENCE      1163 AA;  126691 MW;  6B5F362799417EA4 CRC64;

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Query Match 90.7%; Score 5307; DB 11; Length 1163;
Best Local Similarity 91.1%; Pred. No. 1.7e-258;
Matches 1066; Conservative 34; Mismatches 56; Indels 14; Gaps 7;

Qy	1	MEDIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK	60
Db	1	MEDIDQSSLVSSSADSPRRPPPAFKYQFVTEPEDEEDEEDEE-EEDEDLEEEVLERK	59
Qy	61	PAAGLSAAVPPAAAAPLLDFFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP	120
Db	60	PAAGLSAVPVPP-AAAPLLDFFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAASAPSLP	118
Qy	121	PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAPPPSTPAAPKRRGSGSVDETLFALP	180
Db	119	PAAAVLPSKLPEDDEPPAR--PPAPAGASPLAEPAPPPSTPAAPKRRGSGSVDETLFALP	176
Qy	181	AASEPVIPSSAEKIMDLMEQPNGTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL	240
Db	177	AASEPVIPSSAEKIMDLKEQPNGTVSSGQEDFPSVLFETAASLPSLSPLSTVSFKEHGYL	236

Qy	241	GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSEFKGSPKGES	300
Db	237	GNLSAVASTEGTIEETLNEASRELPERATNPFVNRRESAEFSVLEYSEMGSSEFKGSPKGES	296
Qy	301	AILVENTKEEVIVRSKDKEDLVCSAALHSPQESP-----VGKEDRVVSPEKTMDFNEMQ	355
Db	297	AMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLTKVVKEDGVMSPEKTMDFNEMK	356
Qy	356	MSVVPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLEDSEQKSLGK	415
Db	357	MSVVPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANMESKVDKKCFEDSEQKSHGK	416
Qy	416	DSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKI	475
Db	417	DSESRNENASFPSTPELVKDGSRAYITCDSFTSATESTAANIFPVLEDHTSENKTDEKKI	476
Qy	476	EERKAQIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEA	535
Db	477	EERKAQIITEKTSPKTSNPFLVAIHDEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEA	536
Qy	536	CESELNEATGTKIAYETKVLDLVQTSSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEA	595
Db	537	CESELNEATGTKIAYETKVLDLVQTSSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEA	596
Qy	596	PLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEAMNVALKALGTKEGIK	655
Db	597	PLNSLLPSTGASVAQPSASPLEVPSPVSYDGIKLEPENPPPYEAMSVALKTSDAKEEIK	656
Qy	656	EPESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPHEAELVEDS	715
Db	657	EPESFNAAAQEAAPYISIIACDLIKETKLSTEPSPGFSNYSEIAKFEKSVPDHCELVDDS	716
Qy	716	SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHK-EERLSASPQELGKPY	774
Db	717	SPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVTQHKHKERLSASPQEVGKPY	776
Qy	775	LESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFS	834
Db	777	LESFQPNLHITKDAASNEIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKMKESSETFS	836
Qy	835	DSSPIEIIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSE	894
Db	837	DSSPIEIIIDEFPTFVSAKDDSP---KEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSE	893
Qy	895	KNIYPKDEVHVSDEFSENRSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPS	954
Db	894	KNTYPKDEAHVSDEFKSKRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKKLPS	953
Qy	955	DTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAY	1013
Db	954	DTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAY	1013
Qy	1014	IALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNST	1073
Db	1014	IALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNST	1073
Qy	1074	IKELRRLFLVDDLVDLSLKFAVLMWVFETYVGALFNGLTLLILALISLFSIPVIYERHQVQI	1133


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          |||
Db      1074 IKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQI 1133
QY      1134 DHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
          |||
Db      1134 DHYLGLANKSVKDAMAKIQAKIPGLKRKAE 1163

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RESULT 3

Q8BGK7

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ID      Q8BGK7          PRELIMINARY;          PRT;  1046 AA.
AC      Q8BGK7;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      RTN4.
GN      RTN4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvcJ7, and 129SvcJ7;
RA      Oertle T., van der Putten H., Schwab M.E.;
RT      "Genomic Structure and Functional Characterization of the Promoter
RT      Structures of Human and Mouse Nogo/Rtn-4.";
RL      Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvcJ7, and 129SvcJ7;
RA      Oertle T., Schwab M.E.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvcJ7;
RA      Van der Putten H.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129SvcJ7;
RA      Van der Putten H., Mir A.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AY102280; AAM73502.1; -.
DR      EMBL; AY102286; AAM73507.1; -.
DR      MGD; MGI:1915835; Rtn4.
DR      GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR      GO; GO:0007399; P:neurogenesis; IDA.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
SQ      SEQUENCE  1046 AA;  114221 MW;  8CE2E2238ED51222 CRC64;

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Query Match          77.0%;  Score 4501.5;  DB 11;  Length 1046;
Best Local Similarity 86.9%;  Pred. No. 4.8e-218;
Matches 910;  Conservative 40;  Mismatches 68;  Indels 29;  Gaps 4;

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Qy	143	PPPAGASPLAEPAAPSTPA-----APKRRGSGSVDETLFALPAA	182
Db	3	PPLAGGGQKGGAASEAWVPSLFVGVSGSTCTAAKSLVPIPARSSRLSAARNETLFALPAA	62
Qy	183	SEVPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGN	242
Db	63	SEVPVIPSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLSPLSTVSFKEHGYLGN	122
Qy	243	LSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSEFKGSPKGESAI	302
Db	123	LSAVASTEGTIEETLNEASRELPERATNPFVNRRESAEFSVLEYSEMGSSEFNKSPKGESAM	182
Qy	303	LVENTKEEVIVRSKDKEDLVCSAALHSPQESP-----VGKEDRVVSPEKTMDFNEMQMS	357
Db	183	LVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLTQVVKEDGVMSPEKTMDFNEMKMS	242
Qy	358	VVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLEDSLEQKSLGKDS	417
Db	243	VVAPVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANMESKVDDKKCFEDSLEQKGHGKDS	302
Qy	418	EGRNEDASFPSTPEPVKDSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEE	477
Db	303	ESRNENASFPRTPELVKDGSRAYITCDSFSSATESTANIFPVLEDHTSENKTDEKKIEE	362
Qy	478	RKAQIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACE	537
Db	363	RKAQIITEKTSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEACE	422
Qy	538	SELNEATGTKIAYETKVLDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPL	597
Db	423	SELNEATGTKIAYETKVLDLVQTSEAIQESIYPTAQLCPSFEEAEATPSPVLPDIVMEAPL	482
Qy	598	NSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEP	657
Db	483	NSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEP	542
Qy	658	ESFNAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSP	717
Db	543	ESFNAAQAEAPYISIIACDLIKETKLSTEPSPEFSNYSEIAKFEKSVPDHCELVDSSP	602
Qy	718	ESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-EERLSASPQELGKPYLE	776
Db	603	ESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVTQHKHKERLSASPQEVGKPYLE	662
Qy	777	SFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDS	836
Db	663	SFQPNLHITKDAASNEIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKMKESSETFSDS	722
Qy	837	SPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLLPDLSFKN	896
Db	723	SPIEIIDEFPTFVSAKDDSP---KEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKN	779
Qy	897	IYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDT	956
Db	780	TYPKDEAHVSDEFKSRSSVSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEKKLPSDT	839
Qy	957	EKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIAL	1016

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      |||||:|||||:|||||
Db      840 EKEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIAL 899

Qy      1017 ALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE 1076
      |||||
Db      900 ALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKE 959

Qy      1077 LRRFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHY 1136
      |||||
Db      960 LRRFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHY 1019

Qy      1137 LGLANKSVKDAMAKIQAKIPGLKRKAD 1163
      |||||
Db      1020 LGLANKSVKDAMAKIQAKIPGLKRKAE 1046

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RESULT 4

Q8IUA4

```

ID      Q8IUA4          PRELIMINARY;          PRT;      986 AA.
AC      Q8IUA4;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE      RNT4 (RTN4).
GN      RTN4.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Oertle T., van der Putten H., Schwab M.E.;
RT      "Genomic Structure and Functional Characterization of the Promoter
RT      Structures of Human and Mouse Nogo/Rtn-4.";
RL      Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Oertle T., Schwab M.E.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Van der Putten H.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RX      MEDLINE=22376540; PubMed=12488097;
RA      Oertle T., van der Putten H., Schwab M.E.;
RT      "Genomic Structure and Functional Characterization of the Promoter
RT      Structures of Human and Mouse Nogo/Rtn-4.";
RL      J. Mol. Biol. 325:299-323(2003).
DR      EMBL; AY102285; AAM64244.1; -.
DR      EMBL; AY123245; AAM64249.1; -.
DR      EMBL; AY123246; AAM64250.1; -.
DR      EMBL; AY123247; AAM64251.1; -.
DR      EMBL; AY123248; AAM64252.1; -.
DR      EMBL; AY123249; AAM64253.1; -.

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DR EMBL; AY123250; AAM64254.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;

Query Match 62.0%; Score 3627.5; DB 4; Length 986;
Best Local Similarity 75.4%; Pred. No. 3.9e-174;
Matches 745; Conservative 96; Mismatches 126; Indels 21; Gaps 13;

Qy 195 MDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNL SAVSSSEGTIE 254
||| |||||:|:|||||||||||||||||| |||| ||||| | :||::
Db 1 MDLKEQPGNTISAGQEDFPSVLLETAASLPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQ 60

Qy 255 ETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSFKGSPKGESAILVENTKEEVIVR 314
| ::|||:|:| :||| |||||||||||| ||| ||:| | :||:|:
Db 61 ENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAVIVANPREEIIVK 120

Qy 315 SKDKED-LVCSAALHSPQESVPG-----KEDRVVSPEKTMDFNEMQMSVVAPVREEYAD 368
:||:| | | : ||: || | ||| ||| | | ||| ::| ||:|||||
Db 121 NKDEEEKLVSNILHNQQELPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYAD 180

Qy 369 FKPFEQAWEVKDTYEGSRDLAA----RANVESKVDRKCLEDSEQSLGKDSSEGRNEDA 424
||||: ||||: | | |:|| :|:||||:| | |||| : |||| |:|
Db 181 FKPFERVWEVKDSKEDS-DMLAAGGKIESNLESKVDDKCFADSLEQTNHEKDSSESNDDT 239

Qy 425 SFPSTPEPVKDSSRAYITCASFT-SATESTTANTFPLLEDHTSENKTDEKKIEERKAQII 483
|||||| :|| | ||||| | :||| | |||| | |||||||||:||||:
Db 240 SFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLGDPTSENKTDEKKIEEKKAIQIV 299

Qy 484 TEK-TSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNE 542
||| || |||||||| ||| ||||| |:||| |:|||||||||||||||
Db 300 TEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDLVQEACESELNE 359

Qy 543 ATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLP 602
|||||||||:||||| :||||| |||||||:||||||||||||||| :|
Db 360 VTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVP 419

Qy 603 SAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKAL-GTKEGIKEPESFN 661
|||||:||| |||| |:|:||| |||||||||:|:| | | ||||:|
Db 420 SAGASVIQPSVSPLEA-SSVNYESIKHEPENPPPYEEAMSVSLKKVSGIKEEIKEPENIN 478

Qy 662 AAVQETEAPYISIACDLIKETKLSTEPSDFSNYSEIAKFEKSVPEHAELVEDSSPESEP 721
||:|||||||||||||||||| ||:||||:||||| |: ||:|:||||||:|||
Db 479 AALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDHSSELVEDSSPDSEP 538

Qy 722 VDLFSDDSIPEVPQTQEEAVMLMKESLTVS-ETVAQHK-EERLSASPQELGKPYLESFQ 779
|||||||||:||| |:| |||:||||| | |: :: :|:||| | | |||||||:
Db 539 VDLFSDDSIPDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFK 598

Qy 780 PNLHSTKDA-ASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDDSSP 838
:| :||| ::| |:||||| |||| |:|:||||| ||| |:|:|:|||||||
Db 599 LSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKESAIQIRETETFSDDSSP 658

Qy 839 IEIIDEFFPTFVSAKDDS-PKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNI 897
||||||||| :|:| || |||:||||||| ||||| || |||| ||| ||| |||

Db	659	IEIIDEFPPTLISSKTD SFSKLAREYTDLE VSHKSEIANAPD GAGSLPCTELPHDLSLKN I	718
Qy	898	YPK--DEVHVSDEFSEN RSSVSKASISPSNVSAL EPQTEMGSIVKSKSLTKEAEKKLP SD	955
Db	719	QPKVEEKISFSDDFS KNGSATS KVVLLLPPDV SALATQAEIESIVKPKVLVKEAEKKLP SD	778
Qy	956	TEKEDRSLSAVL SAELSKTSVVDLLYWRDIKKTGVVFGASL FLLLLSLTVFSIVSVTAYIA	1015
Db	779	TEKEDRSPSAIF SAELSKTSVVDLLYWRDIKKTGVVFGASL FLLLLSLTVFSIVSVTAYIA	838
Qy	1016	LALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEVAI SEELVQKYSNSALGHVNSTIK	1075
Db	839	LALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEVAI SEELVQKYSNSALGHVNCTIK	898
Qy	1076	ELRRLFLVDDLVD SLKFVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDH	1135
Db	899	ELRRLFLVDDLVD SLKFVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQVQIDH	958
Qy	1136	YLGLANKSVKDAMAKI QAKIPGLKRKAD	1163
Db	959	YLGLANKNVKDAMAKI QAKIPGLKRKAE	986

RESULT 5

Q7TNB7

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ID      Q7TNB7      PRELIMINARY;      PRT;      720 AA.
AC      Q7TNB7;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6; TISSUE=Brain;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human

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Db 597 PLNSLLPSTGASVAQPSASPLEVSPVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIK 656

Qy 656 EPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDS 715
 ||||| || |||||:|||||:| |||:|

Db 657 EPESFNAAAQAEAPYISIACDLIKETKLSTEPSPEFSNYSEIAKFEKSVDPHCELVDDS 716

Qy 716 SPES 719
 ||| ,

Db 717 SPES 720

RESULT 6

Q8K290

ID Q8K290 PRELIMINARY; PRT; 639 AA.

AC Q8K290;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN RTN4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Strausberg R.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; BC032192; AAH32192.1; -.

DR MGD; MGI:1915835; Rtn4.

DR GO; GO:0005783; C:endoplasmic reticulum; IDA.

DR GO; GO:0007399; P:neurogenesis; IDA.

DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS50845; RETICULON; 1.

KW Hypothetical protein.

SQ SEQUENCE 639 AA; 70312 MW; 309A19DA37603F11 CRC64;

Query Match 50.0%; Score 2926; DB 11; Length 639;

Best Local Similarity 91.6%; Pred. No. 4e-139;

Matches 588; Conservative 20; Mismatches 30; Indels 4; Gaps 2;

Qy 523 MPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEA 582
 |||||:|||||

Db 1 MPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEA 60

Qy 583 TPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEAMN 642
 ||||| ||| ||| ||| |||||:

Db 61 TPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVSPVSYDGIKLEPENPPPYEAMN 120

Qy 643 VALKALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFE 702
 ||| || ||||| || |||||:|||||

Db 121 VALKTSDAKEEIKEPESFNAAAQAEAPYISIACDLIKETKLSTEPSPEFSNYSEIAKFE 180

Qy 703 KSVPEHAELVEDSSPESEPVDFLSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-EE 761
 |||:| |||:||||| |||:|

Db 181 KSVDPHCELVDSSPESEPVDFLSDDSIPEVPQTQEEAVMLMKESLTVSETVTQHKHKE 240

Qy 762 RLSASPQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDL 821
 Db 241 RLSASPQEVGKPYLESFQPNLHITKDAASNEIPTLTKEKISLQMEEFNTAIYSNDDL 300

Qy 822 SKEDKIKESETFSDSSPIEIIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGAD 881
 Db 301 SKEDKMKESETFSDSSPIEIIIDEFPTFVSAKDDSP---KEYTDLEVSNKSEIANVQSGAN 357

Qy 882 SLPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKS 941
 Db 358 SLPCSELPCDLSFKNTYPKDEAHVSDEFKSRSSVSKVPLLLPNVSALESQIEMGNIVKP 417

Qy 942 KSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLS 1001
 Db 418 KVLTKAEAEKKLPSDTEKEDRSLTAVLSAELNKTTSVVDLLYWRDIKKTGVVFGASLFLLLS 477

Qy 1002 LTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQK 1061
 Db 478 LTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQK 537

Qy 1062 YSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFS 1121
 Db 538 YSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFS 597

Qy 1122 IPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163
 Db 598 IPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 639

RESULT 7

Q80W95

ID Q80W95 PRELIMINARY; PRT; 578 AA.
 AC Q80W95;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nogo-A (Fragment).
 GN NOGO-A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tozaki H., Hirata T.;
 RT "The partial sequence of mouse nogo-A cDNA clone#4109.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB073672; BAC75974.1; -.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 FT NON TER 1 1
 SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 44.6%; Score 2610; DB 11; Length 578;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7, and 129SvcJ7;
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvcJ7;
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129SvcJ7;
 RA Van der Putten H., Mir A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY102282; AAM73504.1; -.
 DR EMBL; AY102286; AAM73509.1; -.
 DR MGD; MGI:1915835; Rtn4.
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
 DR GO; GO:0007399; P:neurogenesis; IDA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;

Query Match 24.2%; Score 1416; DB 11; Length 375;
 Best Local Similarity 31.6%; Pred. No. 1.7e-63;
 Matches 367; Conservative 2; Mismatches 6; Indels 788; Gaps 4;

Qy 1 MEDIDQSSLVSSSTDSPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
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 Db 1 MEDIDQSSLVSSSADSPRPPPAFKYQFVTEPEDEEDEEDEE-EEEDDEDLEEEVLERK 59
 Qy 61 PAAGLSAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
 ||||||| || ||||||||||||||||||| ||||||||||| |||||
 Db 60 PAAGLSAAPVPP-AAAPLLDFSSDSVPPAPRGPLPAAPPPTAPERQPSWERSPAASAPSLP 118
 Qy 121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDETFLFALP 180
 ||||||||||| || ||||||||||||||||||| |||||||||||
 Db 119 PAAAVLPSKLPEDDEPPAR--PPAPAGASPLAEPAAPPSTPAAPKRRGSGSVDETFLFALP 176
 Qy 181 AASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
 |||||||||
 Db 177 AASEPVISSA----- 187
 Qy 241 GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSFSGSPKGES 300
 Db 188 ----- 187
 Qy 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360

Db	188	-----	187
Qy	361	PVREEYADFKPFEQAWVEVKDYEGRDVLAAARANVESKVDRKCLEDSEQKSLGKDSEGR	420
Db	188	-----	187
Qy	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTANTFPLEDHTSENKTDEKKIEERKA	480
Db	188	-----	187
Qy	481	QIITEKTS PKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Db	188	-----	187
Qy	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Db	188	-----	187
Qy	601	LPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Db	188	-----	187
Qy	661	NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	188	-----	187
Qy	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	188	-----	187
Qy	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	188	-----	187
Qy	841	IIDEFPFTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	188	-----	187
Qy	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED	960
Db	188	-----	187
Qy	961	RSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 	1020
Db	188	-----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS	232
Qy	1021	VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 	1080
Db	233	VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL	292
Qy	1081	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 	1140
Db	293	FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGLA	352
Qy	1141	NKSVKDAMAKIQAKIPGLKRKAD 	1163

Db 353 NKS VKDAMAKIQA KIPGLKRKAE 375

RESULT 9

Q8BH78

ID Q8BH78 PRELIMINARY; PRT; 356 AA.

AC Q8BH78;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RTN4.

GN RTN4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7, and 129SvcJ7;

RA Oertle T., van der Putten H., Schwab M.E.;

RT "Genomic Structure and Functional Characterization of the Promoter

RT Structures of Human and Mouse Nogo/Rtn-4.";

RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7, and 129SvcJ7;

RA Oertle T., Schwab M.E.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7;

RA Van der Putten H.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=129SvcJ7;

RA Van der Putten H., Mir A.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY102281; AAM73503.1; -.

DR EMBL; AY102286; AAM73508.1; -.

DR MGD; MGI:1915835; Rtn4.

DR GO; GO:0005783; C:endoplasmic reticulum; IDA.

DR GO; GO:0007399; P:neurogenesis; IDA.

DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS50845; RETICULON; 1.

SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match 22.5%; Score 1314.5; DB 11; Length 356;

Best Local Similarity 29.9%; Pred. No. 2e-58;

Matches 348; Conservative 2; Mismatches 6; Indels 807; Gaps 4;

Qy 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60

||||||| :|| |||||

Db 1 MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEEDEE-EEDEDEDLEEEVLERK 59

Qy 61 PAAGLSAAAVPPAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

Db	60	PAAGLSAAPVPP-AAAPLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAASAPSLP	118
Qy	121	PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAPPPSTPAAPKRRGSGSVDETILFALP	180
Db	119	PAAAVLPSKLPEDDEPPAR--PPAPAGASPLAEPAPPPSTPAAPKRRGSGSV-----	168
Qy	181	AASEFVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL	240
Db	169	-----	168
Qy	241	GNLSAVSSSEGTIEETLNEASKELPERATNPFFVNRDLAEFSELEYSEMGSFFKGSPKGES	300
Db	169	-----	168
Qy	301	AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA	360
Db	169	-----	168
Qy	361	PVREEYADFKPFQAWEVKDTYEGSRDVLAAARANVESKVDRCLEDSLEQKSLGKDSEGR	420
Db	169	-----	168
Qy	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTANTFPLLEDHTSENKTDEKKIEERKA	480
Db	169	-----	168
Qy	481	QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Db	169	-----	168
Qy	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Db	169	-----	168
Qy	601	LPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Db	169	-----	168
Qy	661	NAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	169	-----	168
Qy	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	169	-----	168
Qy	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	169	-----	168
Qy	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	169	-----	168
Qy	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED	960

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Db      169 ----- 168
Qy      961 RLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 1020
          |||
Db      169 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLS 213
Qy      1021 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080
          |||
Db      214 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 273
Qy      1081 FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140
          |||
Db      274 FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 333
Qy      1141 NKSVDAMAKIQAKIPGLKRRKAD 1163
          |||
Db      334 NKSVDAMAKIQAKIPGLKRRKAE 356

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RESULT 10

Q8K3G7

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ID   Q8K3G7      PRELIMINARY;      PRT;   357 AA.
AC   Q8K3G7;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nogo-B.
GN   RTN4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Jin W., Li R., Long M., Shen J., Ju G.;
RT   "Cloning and expression of the mouse Nogo-B protein.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY114153; AAM77069.1; -.
DR   MGD; MGI:1915835; Rtn4.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0007399; P:neurogenesis; IDA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   357 AA;  38566 MW;  73BB3D17DFDBDF15 CRC64;

```

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Query Match          22.3%;  Score 1304;  DB 11;  Length 357;
Best Local Similarity 29.9%;  Pred. No. 6.6e-58;
Matches 348;  Conservative 2;  Mismatches 6;  Indels 808;  Gaps 5;

```

```

Qy      1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEEEVLERK 60
          |||
Db      1 MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEEDEE-EEDEDEDLEEEVLERK 59
Qy      61 PAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
          |||

```

Db	60	PAAGLSAAPVPP-AAAPLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAASAPSLP	118
Qy	121	PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAPPPSTPAAPKRRGSGSVDETFLFALP	180
Db	119	PAAAVLPSKLPEDDEPPAR--PPAPAGASPLAEPAPPPSTPAAPKRRGSGSV-----	168
Qy	181	AASEPVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL	240
Db	169	-----	168
Qy	241	GNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSSEFKGSPKGES	300
Db	169	-----	168
Qy	301	AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDIFNEMQMSVVA	360
Db	169	-----	168
Qy	361	PVREEYADFKPFQAWEVKDTYEGSRDVLAAARANVESKVDRKCLEDSELEQKSLGKDSEGR	420
Db	169	-----	168
Qy	421	NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA	480
Db	169	-----	168
Qy	481	QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL	540
Db	169	-----	168
Qy	541	NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL	600
Db	169	-----	168
Qy	601	LPSAGASVVQPSVSPLEAPPVSYDSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF	660
Db	169	-----	168
Qy	661	NAAVQETEAPYISIIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE	720
Db	169	-----	168
Qy	721	PVDLFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHKEERLSASPQELGKPYLESFQP	780
Db	169	-----	168
Qy	781	NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE	840
Db	169	-----	168
Qy	841	IIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK	900
Db	169	-----	168
Qy	901	DEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED	960
Db	169	-----	168

Qy 961 RSLSAVLSAELSKTSVVDLLYWRDIKKTGVV-FGASLFLLLSLTVFSIVSVTAYIALALL 1019
 |||||
 Db 169 -----VVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALL 213

Qy 1020 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR 1079
 |||||
 Db 214 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR 273

Qy 1080 LFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGL 1139
 |||||
 Db 274 LFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGL 333

Qy 1140 ANKSVKDAMAKIQAKIPGLKRKAD 1163
 |||||
 Db 334 ANKSVKDAMAKIQAKIPGLKRKAE 357

RESULT 11

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.
 AC Q96B16;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein (RTN4).
 GN RTN4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Oertle T., Schwab M.E.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Van der Putten H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22376540; PubMed=12488097;
 RA Oertle T., van der Putten H., Schwab M.E.;
 RT "Genomic Structure and Functional Characterization of the Promoter
 RT Structures of Human and Mouse Nogo/Rtn-4.";
 RL J. Mol. Biol. 325:299-323(2003).

DR EMBL; BC016165; AAH16165.1; -.
 DR EMBL; AY102285; AAM64242.1; -.
 DR EMBL; AY102278; AAM64247.1; -.
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match 21.9%; Score 1283.5; DB 4; Length 392;
 Best Local Similarity 29.4%; Pred. No. 8.1e-57;
 Matches 346; Conservative 11; Mismatches 20; Indels 801; Gaps 7;

Qy	1	MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEELEVLERK	60
		: : : :	
Db	1	MEDLDQSPLVSSS-DSPPRQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK	58
Qy	61	PAAGLSAAAVP--PAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAA---P	115
		: : : : : :	
Db	59	PAAGLSAAPVPTAPAAGAPLMDFGNDVPPAPRGPLPAAPPVAPERQPSWDSPVSSTVP	118
Qy	116	APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Db	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPAPAPAAPSTPAAPKR	178
Qy	167	RG-SGSVDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPS	225
Db	179	RGSSGSVDETLFALPAASEPVIRSSA-----	204
Qy	226	LSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEY	285
Db	205	-----	204
Qy	286	SEMGSSFKGSPKGESAILVENTKKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPE	345
Db	205	-----	204
Qy	346	KTMDIFNEMQMSVVAPVREEYADFKPFQAWKDYEGSRDVLAAARANVESKVDRKCLE	405
Db	205	-----	204
Qy	406	DSLEQKSLGKDSEGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPILLEDHT	465
Db	205	-----	204
Qy	466	SENKTDEKKIEERKAQIIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPE	525
Db	205	-----	204
Qy	526	GLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPS	585
Db	205	-----	204
Qy	586	PVLDPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVAL	645
Db	205	-----	204

QY 646 KALGTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDFSNYSEIAKFEKSV 705

Db 205 ----- 204

QY 706 PEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSA 765

Db 205 ----- 204

QY 766 SPQELGKPYLESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKED 825

Db 205 ----- 204

QY 826 KIKESETFSDSSPIEIIDFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPC 885

Db 205 ----- 204

QY 886 LELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLT 945

Db 205 ----- 204

QY 946 KEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF 1005

Db 205 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTVF 234

QY 1006 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 1065

Db 235 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 294

QY 1066 ALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVI 1125

Db 295 ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 354

QY 1126 YERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163

Db 355 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 392

RESULT 12

Q7YRW9

ID Q7YRW9 PRELIMINARY; PRT; 184 AA.

AC Q7YRW9;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RTN4w (Fragment).

GN RTN4.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22715887; PubMed=12832288;

RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;

RT "A reticular rhapsody: phylogenic evolution and nomenclature of the

RT RTN/Nogo gene family.";
 RL FASEB J. 17:1238-1247(2003).
 DR EMBL; AY164744; AAP47319.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 184 AA; 20671 MW; DE990E03BBAF84A1 CRC64;

Query Match 15.0%; Score 878; DB 6; Length 184;
 Best Local Similarity 96.2%; Pred. No. 6.9e-37;
 Matches 177; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 980 LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSD 1039
 |||||
 Db 1 LYWRDIKKTGVVFGXXLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSD 60
 Qy 1040 EGHPPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVF 1099
 |||||
 Db 61 EGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVF 120
 Qy 1100 TYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLK 1159
 |||||:|||||
 Db 121 TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 180
 Qy 1160 RKAD 1163
 |||:
 Db 181 RKA 184

RESULT 13

Q7T224

ID Q7T224 PRELIMINARY; PRT; 199 AA.
 AC Q7T224;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RTN4-C.
 GN RTN4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22715887; PubMed=12832288;
 RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
 RT "A reticular rhapsody: phylogenic evolution and nomenclature of the
 RT RTN/Nogo gene family.";
 RL FASEB J. 17:1238-1247(2003).
 DR EMBL; AY164737; AAP47312.1; -.
 SQ SEQUENCE 199 AA; 22293 MW; 07CF4E4EF2723251 CRC64;

Query Match 15.0%; Score 876; DB 13; Length 199;
 Best Local Similarity 90.6%; Pred. No. 9.7e-37;
 Matches 173; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 973 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1032
 | |||||

Db 9 KDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 68

Qy 1033 QAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSE 1092
 |||||:||||:||||: |||:| |:|||||

Db 69 QAIQKSDEGHPFRAYLESDVAVSEDLIQKYSSVVLGHINGTVKELRRLFLVDDLVDLSE 128

Qy 1093 AVLMMWFTYVGALENGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQ 1152
 |||||:||||| ||||| |:|||||

Db 129 AVLMMWFTYVGALENGLTLLILALISLFSVPVIYERHQAQIDHYLGLVKNVVDAMAKIQ 188

Qy 1153 AKIPGLKRRKAD 1163
 |||||:

Db 189 AKIPGLKRRKTE 199

RESULT 14

Q9GM33

ID Q9GM33 PRELIMINARY; PRT; 179 AA.

AC Q9GM33;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Macaca.

OX NCBI_TaxID=9541;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,

RA Suzuki Y., Sugano S., Hashimoto K.;

RT "Isolation of full-length cDNA clones from macaque brain cDNA

RT libraries.";

RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB049853; BAB16739.1; -.

DR GO; GO:0005783; C:endoplasmic reticulum; IEA.

DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS50845; RETICULON; 1.

KW Hypothetical protein.

SQ SEQUENCE 179 AA; 19949 MW; 5F8CD4383FEE9E02 CRC64;

Query Match 14.4%; Score 844; DB 6; Length 179;

Best Local Similarity 95.5%; Pred. No. 3.4e-35;

Matches 171; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 985 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAIQKSDEGHPF 1044
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRGVQAIQKSDEGHPF 60

Qy 1045 RAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSEFAVLMWFTYVGA 1104
 |||||:||||| |||||:|||||

Db 61 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSEFAVLMWFTYVGA 120

Qy 1105 LFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRRKAD 1163

|||||:|||||:|||||:|||||:
Db 121 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 179

RESULT 15

Q8K4S4

ID Q8K4S4 PRELIMINARY; PRT; 780 AA.
AC Q8K4S4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Reticulon 1A.
GN RTN1 OR RTN-1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Brain;
RA Hirata T., Nomura T., Takagi Y., Sato Y., Tomioka N., Fujisawa H.,
RA Osumi N.;
RT "Mosaic development of the olfactory cortex with Pax6-dependent and -
RT independent components."
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB074899; BAB96551.1; -.
DR MGD; MGI:1933947; Rtn1.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR InterPro; IPR001951; Histone_H4.
DR InterPro; IPR003388; Reticulon.
DR Pfam; PF02453; Reticulon; 1.
DR PROSITE; PS00047; HISTONE_H4; 1.
DR PROSITE; PS50845; RETICULON; 1.
SQ SEQUENCE 780 AA; 83504 MW; 545F5638C576A069 CRC64;

Query Match 13.5%; Score 792; DB 11; Length 780;
Best Local Similarity 32.5%; Pred. No. 1.1e-31;
Matches 242; Conservative 105; Mismatches 260; Indels 138; Gaps 27;

Qy 517 EAAVSNMPEGLTPDLVQEACESELNEATG-----TKIAYETKVDLVQTSEAIQ-ESLY 568
| | : | | : : | | : | : : | : | : : | : :
Db 76 ETASTGM--AAVPDALDHSPSSTLKDGEACYSLSLSDVCYPPREDSAYFTGILQKENGH 133

Qy 569 PTAQLCPSFEEAEATPSPVLPDIVMEAP---LNS-----LLPSAGASVVQPSVSPLEAPP 620
| | | | | | | | : | : | : | : | : | :
Db 134 ITTSESP--EEPE-TPGPSLPEVPGMEPQGLLSSDSGIEMTPAESTEVNKKILADPLDQMK 190

Qy 621 PVSYSIKLE-----PENPPPYEEAMNVALKALGTK-----EGIKEPESFNAAV---- 664
: | : | | | : : | | : | : | : | : | : |
Db 191 AEAYKYIDITRPQEAKGQEEQHPGLEDKDLDFKDKGTEVSTKAEGVRAPNQ-PAPVEGKL 249

Qy 665 -----QETEAPYISIIACDLIKETKLSTEPSPDFSNYSEI-----AKFEKSVPEHAELV 712
: | | | | | : : : | : : | : : | : | : |
Db 250 IKDHLFEESTFAPYIDELSD--EQHRVSLVTAPVKITLTEIEPPLMTATQETIPEKQDLC 307

Qy 713 EDSSPESEPVDFLSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHK-----EERLSASP 767
| : : | : | : : | : | : | : | : | : |

OM protein - protein search, using sw model

Run on: September 3, 2004, 15:58:54 ; Search time 15.4629 Seconds
 (without alignments)
 3916.307 Million cell updates/sec

Title: US-09-830-972-2
 Perfect score: 5848
 Sequence: 1 MEDIDQSSLVSSSTDSPPRP.....VKDAMAKIQAKIPGLKRRKAD 1163

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	5848	100.0	1163	1	RTN4	RAT	Q9jkl1 rattus norv
2	4403.5	75.3	1192	1	RTN4	HUMAN	Q9nqc3 homo sapien
3	917	15.7	199	1	RTN4	MOUSE	Q99p72 mus musculu
4	801	13.7	777	1	RTN1	RAT	Q64548 rattus norv
5	789.5	13.5	776	1	RTN1	HUMAN	Q16799 homo sapien
6	625.5	10.7	236	1	RTN3	HUMAN	O95197 homo sapien
7	625.5	10.7	237	1	RTN3	MOUSE	Q9es97 mus musculu
8	509	8.7	471	1	RTN2	MOUSE	O70622 mus musculu
9	490	8.4	545	1	RTN2	HUMAN	O75298 homo sapien
10	308.5	5.3	5147	1	PCLO	HUMAN	Q9y6v0 homo sapien
11	300	5.1	5120	1	PCLO	CHICK	Q9pu36 gallus gall
12	295.5	5.1	865	1	CPN	DROME	Q02910 drosophila
13	291.5	5.0	2459	1	MAPB	RAT	P15205 rattus norv
14	288	4.9	2468	1	MAPB	HUMAN	P46821 homo sapien
15	284	4.9	2464	1	MAPB	MOUSE	P14873 mus musculu
16	282.5	4.8	2805	1	MAPA	HUMAN	P78559 homo sapien
17	279	4.8	5038	1	PCLO	MOUSE	Q9qyx7 mus musculu

18	277	4.7	3644	1	MINT_MOUSE	Q62504	mus musculu
19	275.5	4.7	3924	1	ANK2_HUMAN	Q01484	homo sapien
20	275	4.7	1972	1	P531_HUMAN	Q12888	homo sapien
21	272.5	4.7	3664	1	MINT_HUMAN	Q96t58	homo sapien
22	272	4.7	5085	1	PCLO_RAT	Q9jks6	rattus norv
23	267	4.6	1781	1	AK12_HUMAN	Q02952	homo sapien
24	265.5	4.5	1828	1	MAP2_MOUSE	P20357	mus musculu
25	261.5	4.5	1087	1	NFH_MOUSE	P19246	mus musculu
26	259.5	4.4	1026	1	NFH_HUMAN	P12036	homo sapien
27	259.5	4.4	2404	1	SON_MOUSE	Q9qx47	mus musculu
28	258.5	4.4	1861	1	MAP2_RAT	P15146	rattus norv
29	257.5	4.4	2715	1	MLL4_HUMAN	Q9umn6	homo sapien
30	256	4.4	1723	1	AIM1_HUMAN	Q9y4k1	homo sapien
31	255.5	4.4	1140	1	YM96_YEAST	Q04893	saccharomyc
32	254.5	4.4	6632	1	UN89_CAEEL	O01761	caenorhabdi
33	254	4.3	1616	1	P200_MYCGE	Q49429	mycoplasma
34	254	4.3	3381	1	PGCV_BOVIN	P81282	bos taurus
35	253	4.3	3421	1	TEGU_HSVEB	P28955	equine herp
36	252.5	4.3	1411	1	TCOF_HUMAN	Q13428	homo sapien
37	252	4.3	2738	1	PGCV_RAT	Q9erb4	rattus norv
38	250.5	4.3	4377	1	ANK3_HUMAN	Q12955	homo sapien
39	248.5	4.2	1189	1	YJH6_YEAST	P47035	saccharomyc
40	248	4.2	1827	1	MAP2_HUMAN	P11137	homo sapien
41	245.5	4.2	1001	1	IF2_SYNY3	P72689	synechocyst
42	244	4.2	1338	1	ACIN_MOUSE	Q9jix8	mus musculu
43	241.5	4.1	8545	1	ANC1_CAEEL	Q9n4m4	caenorhabdi
44	238.5	4.1	831	1	NFH_RAT	P16884	rattus norv
45	238.5	4.1	1341	1	ACIN_HUMAN	Q9ukv3	homo sapien

ALIGNMENTS

RESULT 1

RTN4_RAT

ID RTN4_RAT STANDARD; PRT; 1163 AA.

AC Q9JK11; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)

DE (Glut4 vesicle 20 kDa protein).

GN RTN4 OR NOGO.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.

RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;

RX MEDLINE=99249816; PubMed=10231557;

RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;

RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:

RT a new member of the reticulon family.";

RL Biochim. Biophys. Acta 1450:68-76(1999).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

RX MEDLINE=20129258; PubMed=10667796;
 RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,
 RA Spillmann A.A., Christ F., Schwab M.E.;
 RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
 RT antigen for monoclonal antibody IN-1.";
 RL Nature 403:434-439(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).
 RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;
 RA Ito T., Schwartz S.M.;
 RT "Cloning of a member of the reticulon gene family in rat: one of two
 RT minor splice variants.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP FUNCTION.
 RX MEDLINE=22033691; PubMed=12037567;
 RA GrandPre T., Li S., Strittmatter S.M.;
 RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";
 RL Nature 417:547-551(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults (By
 CC similarity).
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the
 CC membrane of the endoplasmic reticulum through 2 putative
 CC transmembrane domains (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=Nogo-A, NI-220-250;
 CC IsoId=Q9JK11-1; Sequence=Displayed;
 CC Name=2; Synonyms=Nogo-B, Foocen-M1;
 CC IsoId=Q9JK11-2; Sequence=VSP_005658;
 CC Name=3; Synonyms=Nogo-C, VP20;
 CC IsoId=Q9JK11-3; Sequence=VSP_005656, VSP_005657;
 CC Name=4; Synonyms=Foocen-M2;
 CC IsoId=Q9JK11-4; Sequence=VSP_005659;
 CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic
 CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are
 CC present in dorsal root ganglion, sciatic nerve and PC12 cells
 CC after longer exposure. Isoforms 2 and 3 are detected in kidney,
 CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high
 CC level in skeletal muscle. In adult animals isoform 1 is expressed
 CC mainly in the nervous system.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; AF051335; AAF01564.1; -.
 DR EMBL; AJ242961; CAB71027.1; -.
 DR EMBL; AJ242962; CAB71028.1; -.

DR EMBL; AJ242963; CAB71029.1; -.
 DR EMBL; AF132045; AAD31019.1; -.
 DR EMBL; AF132046; AAD31020.1; -.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
 DR GO; GO:0005635; C:nuclear membrane; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
 DR GO; GO:0030517; P:negative regulation of axon extension; ISS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT DOMAIN 1 989 CYTOPLASMIC (Potential).
 FT TRANSMEM 990 1010 POTENTIAL.
 FT DOMAIN 1011 1104 LUMENAL (Potential).
 FT TRANSMEM 1105 1125 POTENTIAL.
 FT DOMAIN 1126 1163 CYTOPLASMIC (Potential).
 FT DOMAIN 976 1163 RETICULON.
 FT DOMAIN 33 46 POLY-GLU.
 FT DOMAIN 73 76 POLY-ALA.
 FT DOMAIN 140 145 POLY-PRO.
 FT VARSPLIC 1 964 Missing (in isoform 3).
 FT /FTid=VSP_005656.
 FT VARSPLIC 965 975 AVLSAELSKTS -> MDGQKKHWKDK (in isoform 3).
 FT /FTid=VSP_005657.
 FT VARSPLIC 173 975 Missing (in isoform 2).
 FT /FTid=VSP_005658.
 FT VARSPLIC 192 975 Missing (in isoform 4).
 FT /FTid=VSP_005659.
 FT CONFLICT 1130 1131 MISSING (IN REF. 3; AAD31020).
 SQ SEQUENCE 1163 AA; 126386 MW; 8CB894B09E94F0B6 CRC64;

Query Match 100.0%; Score 5848; DB 1; Length 1163;
 Best Local Similarity 100.0%; Pred. No. 3.9e-213;
 Matches 1163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEDIDQSSLVSSSTDSPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MEDIDQSSLVSSSTDSPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK 60

 Qy 61 PAAGLSAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 PAAGLSAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPAAPAPSLP 120

 Qy 121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAPPSTPAAPKRRGSGSVDETLEALP 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 PAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAPPSTPAAPKRRGSGSVDETLEALP 180

 Qy 181 AASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 AASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYL 240

 Qy 241 GNLSAVSSSEGTTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSFSGSPKGES 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 GNLSAVSSSEGTTIEETLNEASKELPERATNPFVNRDLAEFSELEYSEMGSFSGSPKGES 300

Qy 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360
 ||||||||||||||||||
 Db 301 AILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPEKTMDFNEMQMSVVA 360
 ||||||||||||||||||
 Qy 361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLEDSELEQKSLGKDSEGR 420
 ||||||||||||||||||
 Db 361 PVREEYADFKPFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLEDSELEQKSLGKDSEGR 420
 ||||||||||||||||||
 Qy 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480
 ||||||||||||||||||
 Db 421 NEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKTDEKKIEERKA 480
 ||||||||||||||||||
 Qy 481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540
 ||||||||||||||||||
 Db 481 QIITEKTSPKTSNPFLVAVQDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESEL 540
 ||||||||||||||||||
 Qy 541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600
 ||||||||||||||||||
 Db 541 NEATGTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSL 600
 ||||||||||||||||||
 Qy 601 LPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF 660
 ||||||||||||||||||
 Db 601 LPSAGASVVQPSVSPLEAPPPVSYSIKLEPENPPPYEEAMNVALKALGTKEGIKEPESF 660
 ||||||||||||||||||
 Qy 661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720
 ||||||||||||||||||
 Db 661 NAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESE 720
 ||||||||||||||||||
 Qy 721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP 780
 ||||||||||||||||||
 Db 721 PVDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQP 780
 ||||||||||||||||||
 Qy 781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE 840
 ||||||||||||||||||
 Db 781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE 840
 ||||||||||||||||||
 Qy 841 IIDEFPPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
 ||||||||||||||||||
 Db 841 IIDEFPPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPK 900
 ||||||||||||||||||
 Qy 901 DEVHVSDEFSENRRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED 960
 ||||||||||||||||||
 Db 901 DEVHVSDEFSENRRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKED 960
 ||||||||||||||||||
 Qy 961 RLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLS 1020
 ||||||||||||||||||
 Db 961 RLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLS 1020
 ||||||||||||||||||
 Qy 1021 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080
 ||||||||||||||||||
 Db 1021 VTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRL 1080
 ||||||||||||||||||
 Qy 1081 FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140
 ||||||||||||||||||
 Db 1081 FLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLA 1140
 ||||||||||||||||||
 Qy 1141 NKSVDAMAKIQAKIPGLKRKAD 1163

|||||
Db 1141 NKS VKDAMAKI QAKIPGLK RKAD 1163

RESULT 2

RTN4_HUMAN

ID RTN4_HUMAN STANDARD; PRT; 1192 AA.
AC Q9NQC3; Q94962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;
AC Q9Y5U6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific
DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).
GN RTN4 OR NOGO OR ASY OR KIAA0886.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20129242; PubMed=10667780;
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,
RA Michalovich D., Simmons D.L., Walsh F.S.;
RT "Inhibitor of neurite outgrowth in humans.";
RL Nature 403:383-384(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=21010696; PubMed=11126360;
RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;
RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on
RT endoplasmic reticulum and reduces their anti-apoptotic activity.";
RL Oncogene 19:5736-5746(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=20237542; PubMed=10773680;
RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;
RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome
RT 2p14-->2p13 by radiation hybrid mapping.";
RL Cytogenet. Cell Genet. 88:101-102(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RA Jin W.-L., Ju G.;
RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC TISSUE=Placenta, and Skeletal muscle;
RA Ito T., Schwartz S.M.;
RT "Cloning of a member of the reticulon gene family in human.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fibroblast;
RA Yutsudo M.;

RT "Isolation of a cell death-inducing gene.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Pituitary;
 RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,
 RA Luo B., Hu R., Chen J.;
 RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
 RA Yu J., Han L.H.;
 RT "Novel human cDNA clone with function of inhibiting cancer cell
 RT growth.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=99156230; PubMed=10048485;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 5:355-364(1998).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
 RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=20499367; PubMed=11042152;
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;

31 December 1998

RT "Cloning and functional analysis of cDNAs with open reading frames for
 RT 300 previously undefined genes expressed in CD34+ hematopoietic
 RT stem/progenitor cells.";
 RL Genome Res. 10:1546-1560(2000).
 RN [12]
 RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).
 RC TISSUE=Brain;
 RA Mao Y.M., Xie Y., Zheng Z.H.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
 RN [13]
 RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RA Sha J.H., Zhou Z.M., Li J.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [14]
 RP TOPOLOGY.
 RC TISSUE=Brain;
 RX MEDLINE=20129259; PubMed=10667797;
 RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;
 RT "Identification of the Nogo inhibitor of axon regeneration as a
 RT Reticulon protein.";
 RL Nature 403:439-444(2000).
 RN [15]
 RP FUNCTION.
 RC TISSUE=Brain;
 RX MEDLINE=21069055; PubMed=11201742;
 RA Fournier A.E., Grandpre T., Strittmatter S.M.;
 RT "Identification of a receptor mediating Nogo-66 inhibition of axonal
 RT regeneration.";
 RL Nature 409:341-346(2001).
 RN [16]
 RP REVIEW.
 RX MEDLINE=21888956; PubMed=11891768;
 RA Ng C.E.L., Tang B.L.;
 RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron
 RT regeneration.";
 RL J. Neurosci. Res. 67:559-565(2002).
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help
 CC block the regeneration of the nervous central system in adults.
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.
 CC This is likely consecutive to their change in subcellular
 CC location, from the mitochondria to the endoplasmic reticulum,
 CC after binding and sequestration.
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum
 CC through 2 putative transmembrane domains.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;
 CC IsoId=Q9NQC3-1; Sequence=Displayed;
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;
 CC IsoId=Q9NQC3-2; Sequence=VSP_005655;
 CC Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;
 CC IsoId=Q9NQC3-3; Sequence=VSP_005652, VSP_005653;
 CC Name=4;
 CC IsoId=Q9NQC3-4; Sequence=VSP_005654;

Db	238	LSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEY	297
Qy	286	SEMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KED	339
Db	298	SEMGSSFVSVPKAEASAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKED	357
Qy	340	RVVSPEKTMDIFNEMQMSVVAPVREEYADFKPFQAWEVKDTYEGSRDVLAA-----RANV	395
Db	358	EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNL	416
Qy	396	ESKVDRKCLEDSEQKSLGKDSEGRNEDASFPSTPEPVKDSGRAYITCASFT-SATESTT	454
Db	417	ESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIA	476
Qy	455	ANTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLS	513
Db	477	TNIFPLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLT	536
Qy	514	KVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQL	573
Db	537	KVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQL	596
Qy	574	CPSFEEAEATPSVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYSIKLEPEN	633
Db	597	CPSFEESEATPSVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPEN	655
Qy	634	PPPYEEAMNVALKAL-GTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDF	692
Db	656	PPPYEEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDF	715
Qy	693	SNYSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS	752
Db	716	SDYSEMAKVEQVPVDPHSELVEDSSPDSEPVDLFSDDSIQDPVQKQDETVMVKESLTETS	775
Qy	753	-ETVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEF	809
Db	776	FESMIEYENKEKLSALPPEGGKPYLESFKLSLNTKDTLLPDEVSTLSKKEKIPLOMEEL	835
Qy	810	NTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVS	868
Db	836	STAVYSNDDLFIKAEQIRETETFSFSDSSPIEIIDEFPTLSSKTDSEFKLAREYTDLEVS	895
Qy	869	DKSEIANIQSGADSLPCLLEPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNV	926
Db	896	HKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDV	955
Qy	927	SALEPQTEMGSIVKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK	986
Db	956	SALATQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIK	1015
Qy	987	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1046
Db	1016	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1075
Qy	1047	YLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1106


```

transmembrane domains (By similarity).
CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=1;
CC          Comment=A number of isoforms may be produced;
CC          Name=1;
CC          IsoId=Q99P72-1; Sequence=Displayed;
CC      -!- SIMILARITY: Contains 1 reticulon domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF326337; AAK08076.1; -.
DR      EMBL; AK003859; -; NOT_ANNOTATED_CDS.
DR      MGD; MGI:1915835; Rtn4.
DR      GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR      GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
DR      GO; GO:0005635; C:nuclear membrane; ISS.
DR      GO; GO:0005515; F:protein binding; ISS.
DR      GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR      GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR      GO; GO:0007399; P:neurogenesis; IDA.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT      DOMAIN      1      25      CYTOPLASMIC (Potential).
FT      TRANSMEM      26      50      POTENTIAL.
FT      DOMAIN      51      137      LUMENAL (Potential).
FT      TRANSMEM      138      162      POTENTIAL.
FT      DOMAIN      163      199      CYTOPLASMIC (Potential).
FT      DOMAIN      12      199      RETICULON.
SQ      SEQUENCE      199 AA; 22466 MW; 07BE5D580059ED9C CRC64;

```

RESULT 4

RTN1_RAT

ID RTN1_RAT STANDARD; PRT; 777 AA.
AC Q64548; Q64547;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Reticulon 1 (Neuroendocrine-specific protein) (S-rex).
GN RTN1 OR NSP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).
RC STRAIN=Wistar; TISSUE=Brain cortex;
RX MEDLINE=96386034; PubMed=8793864;
RA Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,
RA Georgiev G.P., Buchman V.L.;
RT "Intracellular compartmentalization of two differentially spliced s-
RT rex/NSP mRNAs in neurons.";
RL Mol. Cell. Neurosci. 7:289-303(1996).
CC -!- FUNCTION: May be involved in neuroendocrine secretion or in
CC membrane trafficking in neuroendocrine cells.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=RTN1-B; Synonyms=S-RexB;
CC IsoId=Q64548-1; Sequence=Displayed;
CC Name=RTN1-S; Synonyms=S-RexS;
CC IsoId=Q64548-2; Sequence=VSP_005647, VSP_005648;
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND
CC PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS
CC HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.
CC EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL
CC TYPES.
CC -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE
CC HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC
CC DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN
CC THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB
CC DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE
CC HINDBRAIN.
CC -!- SIMILARITY: Contains 1 reticulon domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U17604; AAC53046.1; -.
DR EMBL; U17603; AAC53045.1; -.

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DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT      TRANSMEM      604      624      POTENTIAL.
FT      TRANSMEM      727      747      POTENTIAL.
FT      DOMAIN        590      777      RETICULON.
FT      DOMAIN        610      613      POLY-LEU.
FT      VARSPLIC      1      569      Missing (in isoform RTN1-S).
FT      /FTId=VSP_005647.
FT      VARSPLIC      570      589      IPGPLGSDLVPPLPFENKQK -> MQATADSTKMDCVWSNW
FT      KSQ (in isoform RTN1-S).
FT      /FTId=VSP_005648.
SQ      SEQUENCE      777 AA;  83001 MW;  AF7479C50F28D0AC CRC64;

```

Query Match 13.7%; Score 801; DB 1; Length 777;
Best Local Similarity 32.4%; Pred. No. 2e-23;
Matches 258; Conservative 109; Mismatches 264; Indels 166; Gaps 32;

Qy	485	EKTSPTKSNPFLVAVQDSE-----ADYVTTDTL-----SKVTEAAVSNMPEGL---TPD	530
Db	29	EEATPKGARP---AQQDGEPAWGSGAGAGVVSSRGLCSGPARSPPVAMETASTGVAAVPD	85
Qy	531	LVQEACESELNEATG-----TKIAYETKVDLVQTSEAIQ-ESLYPTAQLCPSFEEAEA	582
Db	86	ALDHSSSPTLKDGEACYSLSIDICYPPREDSAYFTGILQKENGHITTSESP---EELG	142
Qy	583	TPSPVLPDIVMEAPLNSLLPSAGASVVQPS----VSPLEAPPVSYDSIKLE-----	630
Db	143	TPGPSLPEVPGTEP-HGLLSSDSGIEMTPAESTEVNKILADP---LDQMKAEACKYIDIT	198
Qy	631	-----PENPPPYEEAMNVALK----ALGTK-EGIKEPE-----SFNAAVQETE	668
Db	199	RPQEAKGQEEQSPGLEDKDLDFKDKDSEVSTKPEGVHAPNQSPVEGKLIKDNLFEESTF	258
Qy	669	APYISIIACDLIKETKLSTEPSPDFSNYSEI-----AKFEKSVPHEAELVEDSSPESEPD	723
Db	259	APYIDELSD--EQHRMSLVTPVKITLTEIGPPVMTATHETIPEKQDLCIKPSPDTPVTV	316
Qy	724	LFSDDSIPEVPQTQEEAVMLMKESLTEVSETVAQHK-----EERLSASPQELGKPYLESF	778
Db	317	TVSE-----PEDDSPGSVTPPSSGTEPSAAESQKGKGSVSEDELIAAIKEAKGLSYETTE	370
Qy	779	QPN-----LHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETF	833
Db	371	SPRPVGQAADRPVKARSGLPTIPS-----SLDQEASSAESGDSEIELV	414
Qy	834	SDSSPIEIIIDFPT-----FVSAKDDSPKLAK-EYTDLEVSDKSEIANIQSGADSLPCL	886
Db	415	SE-DPMASEDALPSGYVSFGHVSGPPSPASPISQYSILREEREAE-----DSELII	466
Qy	887	ELPCDL-SFKNIYPKDEVH-----VSDEFSENRSSVSKASISPSNVSALEPQTEM---	935
Db	467	E-SCDASSASEESPKREQDSPMKPGVLDAREETSSRATEERAPSHQGPVEPDPILSFT	525
Qy	936	-----GSIV----KSKSLTKEAE----KKLPSDTEKEDRSLSAVLSAEL--	971

[illegible]

RTN1 HUMAN

CC -!- FUNCTION: May be involved in neuroendocrine secretion or in
 CC membrane trafficking in neuroendocrine cells.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=RTN1-A; Synonyms=NSP-A;
 CC IsoId=Q16799-1; Sequence=Displayed;
 CC Name=RTN1-B; Synonyms=NSP-B;
 CC IsoId=Q16799-2; Sequence=VSP_005644;
 CC Name=RTN1-C; Synonyms=NSP-C;
 CC IsoId=Q16799-3; Sequence=VSP_005645, VSP_005646;
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES
 CC AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C
 CC IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.
 CC -!- PTM: Isoforms RTN1-A and RTN1-B are phosphorylated.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; L10333; AAA59950.1; -.
 DR EMBL; L10334; AAA59951.1; -.
 DR EMBL; L10335; AAA59952.1; -.
 DR PIR; A46583; A46583.
 DR PIR; I60904; I60904.
 DR Genew; HGNC:10467; RTN1.
 DR MIM; 600865; -.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; TAS.
 DR GO; GO:0004871; F:signal transducer activity; NAS.
 DR GO; GO:0030182; P:neuron differentiation; TAS.
 DR GO; GO:0007165; P:signal transduction; NAS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;
 KW Phosphorylation.
 FT TRANSMEM 603 623 POTENTIAL.
 FT TRANSMEM 726 746 POTENTIAL.
 FT DOMAIN 589 776 RETICULON.
 FT DOMAIN 609 612 POLY-LEU.
 FT VARSPLIC 1 420 Missing (in isoform RTN1-B).
 FT /FTId=VSP_005644.
 FT VARSPLIC 1 568 Missing (in isoform RTN1-C).
 FT /FTId=VSP_005645.
 FT VARSPLIC 569 588 GPGPLGPGAPPPLLLFLNKQK -> MQATADSTKMDCVWSNW
 FT KSQ (in isoform RTN1-C).
 FT /FTId=VSP_005646.
 SQ SEQUENCE 776 AA; 83617 MW; CA5B6232353096FE CRC64;

Query Match 13.5%; Score 789.5; DB 1; Length 776;
 Best Local Similarity 31.2%; Pred. No. 5.3e-23;
 Matches 243; Conservative 115; Mismatches 252; Indels 169; Gaps 28;

AC 095197;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like
 DE protein II) (NSPLII).
 GN RTN3 OR NSPL2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Retina;
 RX MEDLINE=99265974; PubMed=10331947;
 RA Moreira E.F., Jaworski C.J., Rodriguez I.R.;
 RT "Cloning of a novel member of the reticulon gene family (RTN3): gene
 RT structure and chromosomal localization to 11q13."
 RL Genomics 58:73-81(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou Y., Du G., Yuan J., Qiang B.;
 RT "Cloning and expression analysis of a cDNA encoding a novel
 RT neuroendocrine-specific protein-like protein 1: NSPL1."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Eye, and Lymph;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN
 CC BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL
 CC RETINA.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Reticulon protein 3.
 GN RTN3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang X., Zhou Y., Qiang H., Yuan J., Qiang B.;
 RT "Cloning and expression profile of a novel mouse cDNA encoding a human
 RT RTN3 homolog.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF195940; AAG31360.1; -.
 DR EMBL; BC014697; AAH14697.1; -.
 DR MGD; MGI:1339970; Rtn3.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Transmembrane; Endoplasmic reticulum.
 FT TRANSMEM 69 89 POTENTIAL.

FT TRANSMEM 167 187 POTENTIAL.
 FT DOMAIN 49 237 RETICULON.
 SQ SEQUENCE 237 AA; 25428 MW; EB6QA0A7AC45F0DE CRC64;

Query Match 10.7%; Score 625.5; DB 1; Length 237;
 Best Local Similarity 59.1%; Pred. No. 1.7e-17;
 Matches 114; Conservative 41; Mismatches 37; Indels 1; Gaps 1;

Qy 972 SKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV 1031
 | :| ||::|||:|||| ||| :| :|||| ||::|| :| :| |||||:|||||:| |
 Db 45 SSCAVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRVYKSV 104
 Qy 1032 IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRFLVDDLVDLSLK 1091
 |||:||||:|||||:|||| : : :| | | :| :| :| |||||:|||||
 Db 105 IQAVQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAMVHVNKALKLIIRLFLVEDLVDSLK 164
 Qy 1092 FAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKI 1151
 || ||: |||||:||||:||||| : :||:|:|:|:|:| |||||:|:| | : ||
 Db 165 LAVFMWLMTYVGAVFNGITLLILAEILVFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKI 224
 Qy 1152 QAKIPGL-KRKAD 1163
 |||:||: |:||:
 Db 225 QAKLPGIAKKAE 237

RESULT 8

RTN2_MOUSE

ID RTN2_MOUSE STANDARD; PRT; 471 AA.
 AC O70622; O70620;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like protein 1) (NSPLI).
 GN RTN2 OR NSPL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
 RC STRAIN=FVB/N, and 129/Sv; TISSUE=Cerebellum, and Skeletal muscle;
 RX MEDLINE=98191726; PubMed=9530622;
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
 RT "Molecular cloning of a novel mouse gene with predominant muscle and
 RT neural expression."
 RL Mamm. Genome 9:274-282(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Retina;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum
 CC (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Brain;
 CC IsoId=O70622-1; Sequence=Displayed;
 CC Name=2; Synonyms=Muscle;
 CC IsoId=O70622-2; Sequence=VSP_005650, VSP_005651;
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in neural and muscular
 CC tissues.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF038537; AAC14906.1; -.
 DR EMBL; AF038537; AAC14907.1; -.
 DR EMBL; AF038538; AAC14908.1; -.
 DR EMBL; AF038539; AAC14909.1; -.
 DR EMBL; AF093624; AAD13195.1; -.
 DR EMBL; BC031370; AAH31370.1; -.
 DR MGD; MGI:107612; Rtn2.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane.
 FT TRANSMEM 295 315 POTENTIAL.
 FT DOMAIN 272 471 RETICULON.
 FT VARSPLIC 1 267 Missing (in isoform 2).
 FT /FTId=VSP_005650.
 FT VARSPLIC 268 271 PLLL -> MGSK (in isoform 2).
 FT /FTId=VSP_005651.
 SQ SEQUENCE 471 AA; 51346 MW; 9BBD8F372CF63AD3 CRC64;

Query Match 8.7%; Score 509; DB 1; Length 471;
 Best Local Similarity 28.6%; Pred. No. 1e-12;
 Matches 146; Conservative 84; Mismatches 175; Indels 106; Gaps 13;

Qy 690 PDFSNYSEIAKFEKSVPEHAELVEDSSP--ESEPVDLFSDDSIPEVPQTQEEAVMLMKES 747
 | |:: | |:: | | | | | |::|
 Db 6 PVFAHCKEAPSTASSTPDSTEGNDDSDFRELHTAREFSED----- 46

Qy 748 LTVSETVAQH-----KEERLSASPQELGKPYLESFQPNLHST 785
 | | |:: | : : : | : | | | |
 Db 47 ---EEEETTSQDWGTPRELTFSYIAFDGVVGSGGRRDSVRRRPQGRSVSEPRDPPQSG 104

Qy 786 KDAASNDIPTLTCK-----EKISLQMEEFNTAIYSNDDLSSKEDK 826
 : | |::: |:: |::: : | | |
 Db 105 LGDSLESIPSLSQSPEPGRGDPDPVPPAERPLEELRLRLDQLGWVVR-----AGSGED- 159

Qy 827 IKESETFSDSSPIEIIDEFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCL 886
 | |::: | : | : | | |::: : | |
 Db 160 ----SATSSSTPLE--NEEPDGLLEASE-----AGEETNLEL----RLAQ-----SL 195

Qy 887 ELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKASISPSNVSALEPQTEMGSIVKSKSLTK 946
 | :: : | : | | | : | : | : : : |
 Db 196 HLQLEVLTPQLSPSSGTPQAHTPSPQRSQDSNS--GPDDEPLLNVEEHWRLLLEQEPITA 253

Qy 947 EAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVFS 1006
 : |:: : | : | | | |::: | : | | | |
 Db 254 QC----LDSTDQSEFMLEPLL-----LVADLLYWKDTRTSGAVFTGLMASLLCLLHFS 302

Qy 1007 IVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSA 1066
 | | | | |::: | | | | |::: | : | | | |::: : : : | : : |
 Db 303 IVSVAHLALLGLCATISLRVYRKVLQAVHRGDGTNPQAYLDMDLTLTREQTERLSQQI 362

Qy 1067 LGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIY 1126
 | | | | : | | | | | | | | | | : : | : | | | | | : : | : | : |
 Db 363 ASHVVSTATQLRHFFLVEDLVDLSKLALLFYILTFVGAIFNGLTILVILGVVALFTVPLLY 422

Qy 1127 ERHQVQIDHYLGLANKSVKDAMAKIQAKIPG 1157
 : | | | | | : | : | | | | | |
 Db 423 RQHQAQIDQYVGLVTNQLSHIKAKIRAKIPG 453

RESULT 9

RTN2_HUMAN

ID RTN2_HUMAN STANDARD; PRT; 545 AA.
 AC O75298; O60509;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like protein 1) (NSPLI).
 GN RTN2 OR NSPL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RC TISSUE=Lung carcinoma;
 RX MEDLINE=98360096; PubMed=9693037;
 RA Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;
 RT "cDNA cloning, genomic organization, and expression of the human RTN2

RT gene, a member of a gene family encoding reticulons.";
 RL Genomics 51:98-106(1998).
 RN [2]
 RP SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).
 RC TISSUE=Brain;
 RX MEDLINE=98191726; PubMed=9530622;
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;
 RT "Molecular cloning of a novel mouse gene with predominant muscle and
 RT neural expression.";
 RL Mamm. Genome 9:274-282(1998).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=RTN2-A;
 CC IsoId=075298-1; Sequence=Displayed;
 CC Note=Isoform RTN2-C is produced by alternative initiation at
 CC Met-341 of isoform RTN2-A;
 CC Name=RTN2-B;
 CC IsoId=075298-2; Sequence=VSP_005649;
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced
 CC by alternative initiation at Met-1 and Met-341;
 CC -!- TISSUE SPECIFICITY: ISOFORM RTN2-C IS HIGHLY EXPRESSED IN SKELETAL
 CC MUSCLE.
 CC -!- SIMILARITY: Contains 1 reticulon domain.
 CC -----
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 CC -----
 DR EMBL; AF004222; AAC32542.1; -.
 DR EMBL; AF004223; AAC32543.1; -.
 DR EMBL; AF004224; AAC32544.1; -.
 DR EMBL; AF038540; AAC14910.1; -.
 DR Genew; HGNC:10468; RTN2.
 DR MIM; 603183; -.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; NAS.
 DR GO; GO:0004871; F:signal transducer activity; NAS.
 DR GO; GO:0007165; P:signal transduction; NAS.
 DR InterPro; IPR003388; Reticulon.
 DR Pfam; PF02453; Reticulon; 1.
 DR PROSITE; PS50845; RETICULON; 1.
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;
 KW Alternative initiation.
 FT CHAIN 1 545 RETICULON PROTEIN 2, ISOFORM RTN2-A.
 FT CHAIN 341 545 RETICULON PROTEIN 2, ISOFORM RTN2-C.
 FT INIT_MET 341 341 FOR ISOFORM RTN2-C.
 FT TRANSMEM 368 388 POTENTIAL.
 FT TRANSMEM 463 483 POTENTIAL.
 FT DOMAIN 345 545 RETICULON.
 FT VARSPLIC 272 344 Missing (in isoform RTN2-B).
 FT /FTId=VSP_005649.

SQ SEQUENCE 545 AA; 59263 MW; 971FD2F909E1E9E6 CRC64;

Query Match 8.4%; Score 490; DB 1; Length 545;

Best Local Similarity 28.3%; Pred. No. 6.3e-12;

Matches 160; Conservative 76; Mismatches 202; Indels 128; Gaps 17;

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Qy      668 EAPYISIIACDLIKETKLSTEPSPDFSNYSEI---AKFEKSVPEHAELVEDSSPESEPVDL 724
      |||      | ||| | |:: |:  :| : |  : :|
Db      13 EAP-----STASSTPDSTEGGNDSDSFRELHTAREFSEEDDEEETTSQDWGTPRELTFSY 66

Qy      725 FSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYL-ESFQPNLH 783
      : | :      ::      : ||| || : | | : : | | : | :|
Db      67 IAFDGVVSGGRRDSTARRPRPQGRSVSEPRDQHPQPSLGDSLESI--PSLSQSPEPGRR 124

Qy      784 STKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIEIID 843
      | |      | :      | : |::      | ||      : | |::|
Db      125 GPDPTAP---PSEPLEDLRLRLDHLGWVARGT----GSGED-----SSTSSSTPLE--- 169

Qy      844 EFPTFVSAKDDSPKLAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKNIYPKDEV 903
      | : |      : | || : |      || || : |
Db      170 -----DEEP---QEPNRLLETGEAGE-----EL--DLRLRLAQPSPE 201

Qy      904 HVSDEFSENRRSSVSKASISP-----SNVSALEPQTE----- 934
      :: : |      :      : || || || |
Db      202 VLTPQLSPGSGTPQAGTPSPSRSRDSNSGPEEPLLEEEKQWGPLEREPVRGQCLDSTDQ 261

Qy      935 -----MGSIVK--SKSLTKEAEKKLP-----S 954
      : | : :      ||      | :|
Db      262 LEFTVEPRLLGTAMEWLKTSLLLA VYKTVPILELSPPLWTAIGWVQRGPTPTPVLRVLL 321

Qy      955 DTEKEDRSLSAVLSAELSK---TSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVT 1011
      | || | | | | : | ||||:| : :||| : || | |||||
Db      322 KWAKSPRS-SGVPSLSLGADMGSKVADLLYWKDTRTSGVVFTGLMVSLCLLHFSIVSVA 380

Qy      1012 AYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVN 1071
      |::|| || ||| |::| |::: : | :|||: : : :| : : |
Db      381 AHLALLLLCGTISLRVYRKVLQAVHRGDGANPFQAYLDVDLTLTREQTERLSHQITSRVV 440

Qy      1072 STIKELRRFLVDDLVDSLKFVILMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQV 1131
      | :|| |||:|||||| | :| : : |::|:||||||| : | ||:|::| :||
Db      441 SAATQLRHFFLVEDLVDSLKLALLFYILTFVGAI FNGLTLLILGVIGLFTIPLLYRQHQA 500

Qy      1132 QIDHYLGLANKSVKDAMAKIQAKIPG 1157
      ||| |::|| : |||:|||||
Db      501 QIDQYVGLVTNQLSHIKAKIRAKIPG 526
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RESULT 10

PCLO_HUMAN

ID PCLO_HUMAN STANDARD; PRT; 5147 AA.
AC Q9Y6V0; O43373; O60305; Q9BVC8; Q9UIV2; Q9Y6U9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Piccolo protein (Aczonin) (Fragments).
GN PCLO OR ACZ OR KIAA0559.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 1-759 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99439764; PubMed=10508862;
 RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
 RA Kilimann M.W.;
 RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active
 RT zones, shares homology regions with rim and bassoon and binds
 RT profilin.";
 RL J. Cell Biol. 147:151-162(1999).
 RN [2]
 RP SEQUENCE OF 552-4404 FROM N.A.
 RA Kraemer J., Wollam C., Wohldmann P., McGrane B.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 3619-5147 FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RX MEDLINE=98290545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 RN [4]
 RP SEQUENCE OF 4405-4439 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 4405-5147 FROM N.A.
 RA Kalicki J., Elliott G.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: May act as a scaffolding protein involved in the
 CC organization of synaptic active zones and in synaptic vesicle


```

CC      trafficking (By similarity).
CC      -!- SUBUNIT: Interacts with Rabac1/Pral, RIMS2 and profilin (By
CC      similarity).
CC      -!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of
CC      synaptic junctions (By similarity).
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Comment=Additional isoforms seem to exist;
CC      Name=1;
CC      IsoId=Q9Y6V0-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q9Y6V0-2; Sequence=VSP_003923, VSP_003924, VSP_003925,
CC      VSP_003926, VSP_003927;
CC      Note=No experimental confirmation available;
CC      -!- DOMAIN: C2 domain 1 is involved in binding calcium and
CC      phospholipids. Calcium binds with low affinity but with high
CC      specificity and induces a large conformational change.
CC      -!- SIMILARITY: Contains 2 C2 domains.
CC      -!- SIMILARITY: Contains 1 PDZ/DHR domain.
CC      -----
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CC      -----
DR      EMBL; Y19188; CAB60727.1; -.
DR      EMBL; AC004903; AAD20936.1; -.
DR      EMBL; AC004886; AAD21789.1; -.
DR      EMBL; AB011131; BAA25485.1; -.
DR      EMBL; BC001304; AAH01304.1; -.
DR      EMBL; AC004082; AAB97937.1; -.
DR      PIR; T00634; T00634.
DR      HSSP; P04410; 1A25.
DR      Genew; HGNC:13406; PCLO.
DR      MIM; 604918; -.
DR      GO; GO:0005856; C:cytoskeleton; NAS.
DR      GO; GO:0045202; C:synaptic junction; ISS.
DR      GO; GO:0005509; F:calcium ion binding; ISS.
DR      GO; GO:0005544; F:calcium-dependent phospholipid binding; ISS.
DR      GO; GO:0005522; F:profilin binding; ISS.
DR      GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
DR      GO; GO:0016080; P:synaptic vesicle targeting; ISS.
DR      InterPro; IPR000008; C2.
DR      InterPro; IPR001565; Synaptotagmin.
DR      PRINTS; PR00360; C2DOMAIN.
DR      PRINTS; PR00399; SYNAPTOTAGMN.
DR      SMART; SM00239; C2; 2.
DR      PROSITE; PS00499; C2_DOMAIN_1; 1.
DR      PROSITE; PS50004; C2_DOMAIN_2; 2.
KW      Calcium/phospholipid-binding; Zinc; Metal-binding; Zinc-finger;
KW      Repeat; Alternative splicing.
FT      NON_TER      1      1
FT      DOMAIN      400      465      10 X 10 AA TANDEM APPROXIMATE REPEATS OF
FT      P-A-K-P-Q-P-Q-Q-P-X.

```

FT	ZN_FING	499	523	C4-TYPE (POTENTIAL).
FT	ZN_FING	969	992	C4-TYPE (POTENTIAL).
FT	NON_CONS	1010	1011	
FT	DOMAIN	2300	2325	POLY-PRO.
FT	DOMAIN	4391	4442	PDZ.
FT	DOMAIN	4544	4633	C2 DOMAIN 1.
FT	DOMAIN	5031	5121	C2 DOMAIN 2.
FT	VARSPLIC	4404	4404	S -> SGNGLGIRIVGGKEIPGHSGEIGAYIAKILPGGSAE
FT				QTGKLMEG (in isoform 2).
FT				/FTId=VSP_003923.
FT	VARSPLIC	4534	4534	K -> KPTDGTKVVSHPITGEIQ (in isoform 2).
FT				/FTId=VSP_003924.
FT	VARSPLIC	4576	4576	G -> GQVMVVQNAS (in isoform 2).
FT				/FTId=VSP_003925.
FT	VARSPLIC	4757	4761	TAHKS -> SKRRK (in isoform 2).
FT				/FTId=VSP_003926.
FT	VARSPLIC	4762	5147	Missing (in isoform 2).
FT				/FTId=VSP_003927.
SQ	SEQUENCE	5147 AA;	563537 MW;	CD5D84990498CD3C CRC64;

Query Match 5.3%; Score 308.5; DB 1; Length 5147;
 Best Local Similarity 21.4%; Pred. No. 0.00076;
 Matches 264; Conservative 150; Mismatches 438; Indels 383; Gaps 63;

Qy	3	DIDQSSLVSSSTDSPRRPPPAFKYQFVTEPEDEEDEEEEEDEEDEDLEELEVLERKPA	62
		: : : : : : :	
Db	251	DIVRGESVKPSLSPSPKPP-----IQQPTPGKPPAQQPGHEKSQPG-----PAKPP	296
Qy	63	AGLSAAAVP----PAAAAPLLDFSSDSVPPA-PRGPLPAAPPA-----A	101
		: :	
Db	297	AQPSGLTKPLAQPGTVKPPVQPPGTTKPPAQPLG--PAKPPAQQTGSEKPSSEQPGPKA	354
Qy	102	PERQPSWERSPA-APAPSLP-----PAAAVLPSKLPEDDEPPA---	138
		: : : : : : :	
Db	355	LAQPPGVGKTPAQQPGPAKPPTQQVGTPKPLAQQPGQLQSPAKAPGPTKTPAQTKPPSQQP	414
Qy	139	---RPPPPPPAGASPLAEPAPPPSTPAAPKRRGSGSVDETFLFALPAASEPVPISSAEKIM	195
		: : : : :	
Db	415	GSTKPPPPQPGPAKP--SPQQPGSTKPPSQPGS-----AKPSAQQ---PSPAKPSA	461
Qy	196	DLMEQPGNTVSSGQEDFPSVLLETAASLPS-----LSPL-STVSFKEH-GYLGNLSAVS	247
		: : : : : : : : :	
Db	462	QQFTKPVSQTGF GKPLQPPTVSPSAKQPPSQGLPKTICPLCNTTELLLVPEKANFNTCT	521
Qy	248	SSEGTI-----EETLNEASKEL-----PERATNPFVNRDL	277
		: : : : :	
Db	522	ECQTTVCSLCGFNPNPHLTEAKEWLCLNCQMKRALGGDLAPVPSSPQPKLTAPVTTTSA	581
Qy	278	AEFSELEYSEMGSSFFKGS PKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGK	337
		: : : : : : : : :	
Db	582	VSKSSPQPQQTSPKKDAAPKQDLKAPEPKPPPLVKQPTLHGSPSAKAKQPPEADSLSK	641
Qy	338	EDRVVSPEKTMDFNEMQMSVAVPVREEYADFKPFQAWVEVKDYEGRDVLAAARANVES	397
		: : : : : :	
Db	642	P----APPKEPSVPSEQDK---APV----ADDKP-KQPKMVKPTTD---LVSSSSATTKP	686
Qy	398	KVDRKCLEDLSLEQKS---LGKDSEGRNEDASFPSTPEPVKDSRAYITCASFTSATESTT	454

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      :      :: |::: | ||      :: ||| || | | | | | |
Db    687 DIPSSKVQSQAEKTTPLKTD SAKPSQ--SFPPTGEKV-----TPFDSKAIPRP 734

Qy    455 ANTFPLLE--DHTSENKTD-----EKKIEERKAQIITEKTS PK----- 490
      |:      ::      :||:|      :|| | :||| | |||
Db    735 ASDSKIISHPGPSSESKGQKQVDPVQKKEEPKKAQ--TKMSPKPDAPMPKGSPTPPGP 791

Qy    491 --TSNPFLVAVQDS----EADYVTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEAT 544
      |:      : | | |      : | :|| | | | | | | |
Db    792 RPTAGQTVPTPQQSPKPEQSRFSLNLGSITDAPKSQ-----PTTPQET-----VT 838

Qy    545 GTKIAYETKVDLVQTSEAIQESLYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSA 604
      | :      : | | | : | | : | | : :|| | | :|:
Db    839 GKLFGFGASI-FSQASNLISTAGQPG----PHSQSGPGAP-----MKQAPAPSQPPTS 886

Qy    605 GASVVQPSVSPLEAPP-----PVS YD-----SIKLEP-----ENPPPYEE 639
      | | :||| || :      : ||| | | | | : ||| ::
Db    887 QG----PPKSTGQAPPAPAKSIPVKKETKAPAAEKLEPKAEQAPTVKRTETEKKPPPIKD 942

Qy    640 AMNVALK----ALGTK-----EGIKEPESFNAAVQ-----E 666
      : ::      : | | | | | | | | | | | | : || : ||
Db    943 SKSLTAEPQKAVLPTKLEKSPKPESTCPLCKTELNIGSKDPPNFNTCTECKNQVCNLCGF 1002

Qy    667 TEAPYISIA C-----DLIK-----ETKLSTEPSPDFS NYSEIAKFEKSVPEHA 709
      |::: | | : | | | | | | : | : : :||
Db    1003 NTPPHLTENCQTQRAISGQLGDIRKMPPAPSGPKASMPVP-----TESSSQKTAVPPQV 1057

Qy    710 ELV----EDSSPESEPV-----DLFSDDSIPEV---PQTQEEAVMLMKESLTEVSETVA 756
      :||      :: |::| | : | : || : | ||| : | | : : |
Db    1058 KLVKKQEVEVKTEAEKVILEKVKETLSMEKIPPMVTTDQKQEE S-KLEKDKASALQEKKP 1116

Qy    757 QHKEERLSASPQEL----GKPYLESFQPNLHSTKDAASNDIPTLT KKEKISLQMEEFNTA 812
      :|::|      :: | | | | : | | | : | | | :|
Db    1117 LPEEKKLIPEEEKIRSEEKPLLEEKKPTPEDKK-----LLPEAKTSAPEEQ---- 1163

Qy    813 IYSNDDLSSK----EDKI-----KESETFSDSSPIEIIDEFPTFVSAKDDS- 855
      ||| | : | : | : | : | : | : | : | : ||
Db    1164 ---KHDLLKSQVQIAEEKLEGRVAPKTVQEGKQPQTKMEGLP----SGTPQSLPKEDDKT 1216

Qy    856 -----PKLAKEYTDLEVSDKSEIANIQ-----SGADSLPCLELPCD 891
      | || : | ||| : : | | | | | | | :|
Db    1217 TKTIKEQPQPCTAKPDQKEE-DDKSDTSSSQPKSPQGLSDTGYSSDGISSSLGEIP-- 1273

Qy    892 LSFKNIYPKDEVHV----SDEFSENRRSSVSK---ASISPSNVSALEPQTEMGSIVKSKS 943
      : : | || : | ||| : | | | : : : | || | : ||:
Db    1274 ----SLIPTDEKDILKGLKKDSFSQESSPSSPSDLAKLESTVLSILEAQASTLADEKSEK 1329

Qy    944 LTK--EAEKKLPDTEKEDRSLSAVLSAELSKTSV 976
      |: | : | | || :||| | :|: :
Db    1330 KTOPHEVSPEQPKDQEK-TQSLSETLEITISEEEI 1363

```

RESULT 11

PCLO_CHICK

ID PCLO_CHICK STANDARD; PRT; 5120 AA.

AC Q9PU36;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Piccolo protein (Aczonin) (Fragment).
 GN PCLO OR ACZ.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99439764; PubMed=10508862;
 RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
 RA Kilimann M.W.;
 RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active
 RT zones, shares homology regions with rim and bassoon and binds
 RT profilin.";
 RL J. Cell Biol. 147:151-162(1999).
 CC -!- FUNCTION: May act as a scaffolding protein involved in the
 CC organization of synaptic active zones and in synaptic vesicle
 CC trafficking (By similarity).
 CC -!- SUBUNIT: Interacts with Rabac1/Pral and profilin (By similarity).
 CC -!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of
 CC synaptic junctions (By similarity).
 CC -!- DOMAIN: C2 domain 1 is involved in binding calcium and
 CC phospholipids. Calcium binds with low affinity but with high
 CC specificity and induces a large conformational change.
 CC -!- SIMILARITY: Contains 2 C2 domains.
 CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
 CC -----
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 CC -----
 DR EMBL; Y19187; CAB60725.1; -.
 DR HSSP; P04410; 1A25.
 DR GO; GO:0045202; C:synaptic junction; ISS.
 DR GO; GO:0005509; F:calcium ion binding; ISS.
 DR GO; GO:0005544; F:calcium-dependent phospholipid binding; ISS.
 DR GO; GO:0005522; F:profilin binding; ISS.
 DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
 DR GO; GO:0016080; P:synaptic vesicle targeting; ISS.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR001478; PDZ.
 DR InterPro; IPR001565; Synaptotagmin.
 DR InterPro; IPR008899; Znf_piccolo.
 DR Pfam; PF00168; C2; 2.
 DR Pfam; PF00595; PDZ; 1.
 DR Pfam; PF05715; Zf_piccolo; 2.
 DR PRINTS; PR00399; SYNAPTOTAGMN.
 DR SMART; SM00239; C2; 2.
 DR SMART; SM00228; PDZ; 1.

DR PROSITE; PS00499; C2_DOMAIN_1; 1.
 DR PROSITE; PS50004; C2_DOMAIN_2; 2.
 DR PROSITE; PS50106; PDZ; 1.
 KW Calcium/phospholipid-binding; Zinc; Metal-binding; Zinc-finger;
 KW Repeat.
 FT NON_TER 1 1
 FT DOMAIN 258 357 10 X 10 AA TANDEM APPROXIMATE REPEATS OF
 FT P-A-K-P-Q-P-Q-Q-P-X.
 FT ZN_FING 368 392 C4-TYPE (POTENTIAL).
 FT ZN_FING 836 859 C4-TYPE (POTENTIAL).
 FT DOMAIN 2324 2343 POLY-PRO.
 FT DOMAIN 4414 4493 PDZ.
 FT DOMAIN 4627 4726 C2 DOMAIN 1.
 FT DOMAIN 5003 5094 C2 DOMAIN 2.
 SQ SEQUENCE 5120 AA; 560751 MW; A658D9891B65B412 CRC64;

Query Match 5.1%; Score 300; DB 1; Length 5120;
 Best Local Similarity 20.4%; Pred. No. 0.0016;
 Matches 258; Conservative 152; Mismatches 464; Indels 388; Gaps 56;

Qy 14 TDSPPRPPPAFKYQFVTEPEDEEDEEE-----EEDDEEDDEDLEELVLERKPAAGLSAA 68
 :|| | : | ||: | : ||: : : : : : : | : |
 Db 90 SDSDAAEHEEAGRKQKVTQKEQGKPEEQRGLAKHPSQQQSPKLVQQQGPVKPTPQQTESSK 149
 Qy 69 AVP-----PAAAAPLLDFSSDSV--PPAPRGP----LPAAPPAAPERQPSWE 109
 || | : | | : : | || ||| | : | | : | :
 Db 150 PVPQQQQPGEPKQGQKPGPSHP-GDSKAEQVKQPQPRGPQKSQLOQSEPTKPGQQQTSA 208
 Qy 110 RSPAAPAPSLP--PAAAVLPSKLPEDDEP-----PAR-----P 140
 : : | | || | : | : | : | || | |
 Db 209 KTSAGPTKPLPQQPDSAKTSSQAPPPTKPSLQQSGSVKQPSQQPARQGGPVKPSAQQAGP 268
 Qy 141 PPPPPAGASPLAEPAAPPSTPAAPKRRGSGSVDET--LFALPAASEPVIPISS--AEKIMD 196
 | | | | : | | | | : : | : : | | | |
 Db 269 PKQQPGSEKPTAQQTGPAKQPPQP-GPGKTPLOQTGPVKQVPPQAGPTKPSQTAGAAS 327
 Qy 197 LMEQPGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNL SAVSSSEG TIEET 256
 | : ||| | -||: | | : : : | | | : |
 Db 328 LAQQPGLTKPPGQQPGPEKPLQQKQA-----STTQPVESTPKKT 366
 Qy 257 L-----NEASKELPERAT-----NPFVNRDLAEFSE-----LEYS 286
 | ||: | || | : | | : :
 Db 367 FCPLCTTTTELLLTPEKANYNTCTQCHTVVCSLCGFNP--NPHITEIKEWLCCLNCQMORA 424
 Qy 287 EMGSSFKGSPKGESAILVENTKEEVIVRSKDKEDLVCSAALHSPQESPVGKEDRVVSPE- 345
 | | | : | | | | | | : | :
 Db 425 LGGDLASGHGPGPQ-----LPPPKQKTPTPASTAKPSPQLQPGQKKDASPKPDP 473
 Qy 346 -----KTMDIFNEMQMSVVAPVREEYADFKPFEQAWVKDTYEGSRDVLAAARANVESK 398
 | : : | ||: : : | : : | : | : |
 Db 474 SQQADSKKPVPQKKQPSMPGSPVKSQKQTHAEPSTGQQI-DSTPKSDQVKPTQA----- 527
 Qy 399 VDRKCLEDLSLEQKSLGKD-----SEGRNEDASFPSTPEPVKDSSRAYITCASFTSA 449
 | : | | : | : | : | : | : | : | :
 Db 528 -----EEKQNQPSIQKPTMDTVPTSAAPGVKQDLADFPQSP-----STQQKVTDSMPMPET 576
 Qy 450 TESTTANTFPLLEDHTSENKTDEKKIEERKAQIITEKTSP-----KTSNPFVLV 497

Db	577	TK-----PPADTHPAGDPKPDSKPL-----PQVSRQKSDPKLASQSGAKSDAKTQKPSEP	625
Qy	498	A-VQDSEADYVT-----TDTLSKVTEAAVSNMPE-----	525
Db	626	APVKDDPKKLQTKPAPKPDTPAPKGPQAGTGPRPTSAQPAPQPQQPQKTPEQSRRFSLN	685
Qy	526	--GLT-----PDLVQEACESEL-----NEA-----TGTKIAYETKVDLVQTSEAIQ	564
Db	686	LGGITDAPKPQPTTPQETVTGKLFGFGASIFSQASSLISTAGQPGSQTSGBPAPPATKQPQ	745
Qy	565	ESLYPTAQLCPSFEEAEATPSP-VLPDIVMEAPLNS--LLPSAGASVVQPSVSPLEAPPP	621
Db	746	PPSQPPASQAPPKEAAQAQPPPKAAPTKKETKPLASEKLGPMASDSTLTTKGSDLEKKPS	805
Qy	622	VSYDSIKLEPENPPPYE-----EAMNVALKALGTKEGIKEPESFNAA-----	663
Db	806	LAKDSKHQTAEAKKPAELSEQEKASQPKVSCPLCKTGLNIGSKDPPNFNTCTECKKVVCN	865
Qy	664	-----VQETEAPYISIA-----DLIK-----	680
Db	866	LCGFNPMPHIVEVQE---WLCLNCQTQRAMSGQLGDMGKVPLPKLGPSQPVSKPPATPQ	921
Qy	681	-----ETKLSTEPSPDFSNYSEIAKFEKSVP--EHAEL-----VEDSS	716
Db	922	KQVPVAVSHSPQKSSTPPTPAATKPKKEPSVPKEVPKLQQGKLEKTLADKIQQGIQKED	981
Qy	717	PESEPVDLF---SDDSIPEVPQTQEEAVMLMKESLTVSETVAQH-KEERLSASPQELGK	772
Db	982	AKSKQGKLFKTPSADKIQRVSQKEDSRLQOTKLTPTSSDKILHGVQKEDIKFQEAKLAK	1041
Qy	773	-----PYLESFQPNLHSTKDA---ASNDIPTLTKEKISLQMEEFNTAIYSN-----	816
Db	1042	IPSADKILHRLQKEDPKLQQMKMAKALSADKIQPEAQKEDVQLQEVRLSKAVSADKIQHG	1101
Qy	817	--DDL-----LSSKEDKI---KESETFSDSSPIEII-DEFPTFVSA-----	851
Db	1102	IQKDLNLQHVKIEKTSSVEKIQEAQKESKLQQDKLPKTLSEDKIPATVSSDHKKLLSKSE	1161
Qy	852	KDDSPKLAKEYTDLEVSDKSEIANIQSG--ADSLPCLELPCDLSFKNIYPKDEVHVSDE-	908
Db	1162	EDKKPELLEKSTPHPKDKKEQITAETTGHITEQKVEVEAPCD---KLHEKKQEDVKKED	1217
Qy	909	----FSENRSSVSKA--SISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRS	962
Db	1218	LTTGIPQMVSKEPEAAEEKTPVPVPSRL-PRSDHVEAVREK-IEKEDDK---SDTSSSQQQ	1272
Qy	963	LS 964	
Db	1273	KS 1274	

RESULT 12

CPN_DROME

ID CPN_DROME STANDARD; PRT; 865 AA.

AC Q02910;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Calphotin.
 GN CPN OR CAP.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=93165729; PubMed=8094559;
 RA Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
 RT "Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S;
 RX MEDLINE=93165730; PubMed=8434015;
 RA Ballinger D.G., Xue N., Harshman K.D.;
 RT "A Drosophila photoreceptor cell-specific protein, calphotin, binds
 RT calcium and contains a leucine zipper.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).
 CC -!- FUNCTION: Might function as a calcium-sequestering "sponge" to
 CC regulate the amount of free cytoplasmic calcium. It binds 0.3 mole
 CC of Ca(2+) per mole of protein.
 CC -!- SUBUNIT: Homodimer (Probable).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic; hypodense compartment.
 CC -!- TISSUE SPECIFICITY: Soma and axons of photoreceptor cells of
 CC compound eyes and ocelli.
 CC -!- DEVELOPMENTAL STAGE: Expressed early in photoreceptor cell
 CC development.

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 CC -----

DR EMBL; L02111; AAA28405.1; -.
 DR EMBL; L05080; AAA28420.1; -.
 DR PIR; A47282; A47282.
 DR PIR; A47283; A47283.
 DR FlyBase; FBgn0010218; Cpn.
 DR GO; GO:0005509; F:calcium ion binding; IDA.
 KW Calcium-binding.
 FT CONFLICT 36 36 A -> AVAPAVVA (IN REF. 2).
 FT CONFLICT 43 43 I -> T (IN REF. 2).
 FT CONFLICT 64 64 I -> V (IN REF. 2).
 FT CONFLICT 76 76 T -> A (IN REF. 2).
 FT CONFLICT 100 100 P -> PP (IN REF. 2).
 FT CONFLICT 126 127 VQ -> AP (IN REF. 2).
 FT CONFLICT 154 154 I -> V (IN REF. 2).
 FT CONFLICT 160 160 S -> T (IN REF. 2).

FT CONFLICT 534 534 A -> E (IN REF. 2).
 FT CONFLICT 699 699 I -> T (IN REF. 2).
 FT CONFLICT 703 703 V -> L (IN REF. 2).
 FT CONFLICT 721 721 D -> E (IN REF. 2).
 SQ SEQUENCE 865 AA; 84781 MW; 2110417E0B0E7CFE CRC64;

Query Match 5.1%; Score 295.5; DB 1; Length 865;
 Best Local Similarity 21.3%; Pred. No. 0.00024;
 Matches 217; Conservative 127; Mismatches 379; Indels 295; Gaps 41;

Qy	62	AAGLSAAAVPPAAAAPLLDSSDSVPPAPRGPLPAAPPAAPER----	QPSWERSPAAPAP	117
		: :: : : : :		
Db	11	SAPVAAPVTTPSAVAAPVQVVSPAAPVAPAAPIAVTPVAPPPTLASVQPATVTIP-APAP		69
Qy	118	----SLPPAAAVLPSKLPEDDEPPARPPPPPPAGA-----	SPLAEPAAAPPSTP-----	161
		: : : : :		
Db	70	IAAASVTPVASVAPPVVAAPTTPAASPVSTPVAVAQIPVAVSAPVAPPVVAATPTPVVQIP		129
Qy	162	-AAPKRRGSGSVDETLFALP--AASEP----VIPSSAEKIMDLMEQPGNT---	VSSGQED	211
		: : : :		
Db	130	VAAP-----VIATPPVAASAPTPAAVTPVISPVIASPPVVPANTTVPVAAAPVAA		178
Qy	212	FPSVLLETAASL-PSLSPLSTVSFKEHGYLGNL SAVSSSEG TIEETLNEASKELPERATN		270
		: : : : : : : : :		
Db	179	VPAAPVPVAPVLAPAVAPAVAPVVAETPAPPPVAEIPVA--TIPECVAPLIPEVSVVATK		236
Qy	271	PFVNRDLAEFSELEYSEMGS SFKGS PKGESAILVENTKEEVIVRSKDKEDLVCSAALHSP		330
Db	237	PLA-----AAEPVVVAPPATETPVVAPAAAASP		263
Qy	331	QESPVGKEDRVVSPEKTMDIFNEMQMSV VAPVREEYADFKPF EQAWEVKD TYEGSRD VLA		390
		: : : :		
Db	264	HVS-----VAP-----AVETAVVAPV-----		279
Qy	391	ARANVESKVDRKCLED SLEQKSL----GKDSEGRNEDASFPSTPEPVKDSSRAYITCASE		446
		: : : : : : : :		
Db	280	-SASTEPPVAAATLT TAPETPALAPVVAESQVAANTVVATPPTPAPEPETIAPPVVAETP		338
Qy	447	TSATESTTANTFPLLEDHTSENKTDEKKIEERKAQIITEKTS PKTSPNFLVAVQDSEADY		506
		: : : : : : : :		
Db	339	EVASVAVAETTPPVVPPVAAES-----IPAPVVATTVPVATLAVTDPD---		381
Qy	507	VTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATG TKIAYETKVDLVQTSEAIQES		566
		: : :		
Db	382	-----VTASAVPELPPVIA PSPVPSA-----VAETPVDLA-----PPV		414
Qy	567	LYP-TAQLCPSF--EEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAP----		619
		: : : : : :		
Db	415	LPPVAAEPVPAVVAEETPETPAPASAPVTI-AALD--IPEVAPVIAAPSDAPAEAPSAAA		471
Qy	620	PPVSYDSIKLEPENPPPPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIIACD--		677
		: : :		
Db	472	PIVS-----TPPT-----TASVPETTAPPAAVPTEPI		498
Qy	678	---LIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAE--LVEDSSPESEPVDLFSD-DSIP		731
		: : : : : : : : :		
Db	499	DVSVLSEAAIETPVAPPVEVTTEVAVADVAPPEAAADLII EPVEPPAPIPD LLEQTTSVP		558

Qy	732	EVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYLESFQPNLHSTKDAASN	791
		: : : : : : : : : : : :	
Db	559	AVEAAESTSSPIPETSLPPPNEAVA--SPEVAVAPITAPEPIPEP-EPSLATPTEPIPV	614
Qy	792	DIPTLTKKKIKISLQMEEFNTAIYSNDDLSSKEDIKIKESETFSDSSPIEIIDEFPTFVSA	851
		: : : : : : : : : : : : :	
Db	615	EAPV-----VIQEAVDAVEVPVTETSTSIPEPTEVEFPEAVAE	651
Qy	852	KDSPKLAKEYTDLEV-SDKSEIANIQSGAD---SLPCLEL-----PCDLSFKNIYP-	899
		: : : : : : : : : :	
Db	652	KVLDPAI----TEAPVTTQEPDVANINDGAPATEITTPAVEIVTAAAEVSDIAIPVIDPP	707
Qy	900	-KDEVHVSDEFSENRRSSVSKASISPSNVSALEPQTEMG-----	936
		: : : : : : : :	
Db	708	VPQEIAVA-EIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAAEVPITAGDN	766
Qy	937	----SIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKKTGV	990
		: : : : : : : :	
Db	767	PDNTSVGISEVVPPTIAEKPVEEVPTSEIPEOSSSPSDSVPVAKITPLL--RDLQTTDV	822

MAPB RAT

RA Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.;
 RT "Neuraxin, a novel putative structural protein of the rat central
 RT nervous system that is immunologically related to microtubule-
 RT associated protein 5.";
 RL EMBO J. 8:2879-2888(1989).
 RN [4]
 RP DEVELOPMENTAL STAGE, AND PHOSPHORYLATION.
 RX MEDLINE=97405699; PubMed=9260743;
 RA Ma D., Nothias F., Boyne L.J., Fischer I.;
 RT "Differential regulation of microtubule-associated protein 1B (MAP1B)
 RT in rat CNS and PNS during development.";
 RL J. Neurosci. Res. 49:319-332(1997).
 CC -!- FUNCTION: The function of brain MAPS is essentially unknown.
 CC Phosphorylated MAP1B may play a role in the cytoskeletal changes
 CC that accompany neurite extension. Possibly MAP1B Binds to at least
 CC two tubulin subunits in the polymer, and this bridging of subunits
 CC might be involved in nucleating microtubule polymerization and in
 CC stabilizing microtubules.
 CC -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
 CC with MAP1A and MAP1B proteins.
 CC -!- TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem,
 CC cerebellum and cerebrum). Not expressed in liver, spleen, kidney,
 CC heart or muscle.
 CC -!- DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic
 CC nerve levels are high early in development but decrease during
 CC postnatal development and are low in adults. In dorsal root
 CC ganglia levels remain high throughout development.
 CC -!- INDUCTION: By nerve growth factor.
 CC -!- DOMAIN: Has a highly basic region with many copies of the sequence
 CC KKEE and KKEI/V, repeated but not at fixed intervals, which is
 CC responsible for the binding of MAP1B to microtubules.
 CC -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
 CC from MAP1B by proteolytic processing. It is free to associate with
 CC both MAP1A and MAP1B. It interacts with the amino-terminal region
 CC of MAP1B (By similarity).
 CC -!- PTM: Phosphorylated.
 CC -!- SIMILARITY: TO MAP1A.
 CC -!- CAUTION: A C-terminal fragment of this protein (residues 1597 to
 CC 2459) was originally described as neuraxin in Ref.3.
 CC -----
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 CC -----
 DR EMBL; U52950; AAB17068.1; -.
 DR EMBL; X60370; CAC16162.1; -.
 DR EMBL; X16623; CAA34620.1; ALT_SEQ.
 DR PIR; A56577; A56577.
 DR InterPro; IPR000102; MAP1B_neuraxin.
 DR Pfam; PF00414; MAP1B_neuraxin; 10.
 DR PROSITE; PS00230; MAP1B_NEURAXIN; 8.
 KW Microtubule; Repeat; Phosphorylation.
 FT CHAIN ? 2459 MAP1 LIGHT CHAIN LC1.


```

      |   :|   :   |   |   | :| :| :| |   ||:|:
Db      1439 D-----LTSDLYQDKQEEKRAGFIPIKEDFSPEKKASDAEIMSSQSALALDERKLGGDGS 1493

Qy      476 -----EERKAQIITEKTSNPKTSNPFLLVAVQDSEADYVTTDTLSKVTEAAV-- 520
      | :| | | | | :| :| :| :| :| :| :| :|
Db      1494 PTQVDVSQFGSFKEDTKMSISEGTVSDKSATPVDEGAEDT---YSHMEGVASVSTASVAT 1550

Qy      521 SNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQES-LYPTAQLCP---S 576
      | :| | | | : :| :| :| :| | | :| :| :| |
Db      1551 SSFPEPTTDD-VSPSLHAEVGSPPHSTEVDSSLSVSVVQTPPTTFQETEMSPSKEECPRMS 1609

Qy      577 FEEAEATP-----SPVLPDIVMEAPLNSLL-----PSAGASVVQ 610
      : :| | : :| :| :| :| :| :| :| :| :|
Db      1610 ISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSLAMDFSRQSPDHPTVGAGMLH 1669

Qy      611 PSVSPLEAPPPVSYD-----SIKLEPENPPPYEEAMNVALKALGTKEGIKEPESFN 661
      : : | | | | :| :| | :| :| :| :| :| :| :| :|
Db      1670 ITEN---GPTEVDYSPSDIQDSSLHKIPPTTEPSYTDNDLS-ELISVSQVEASPSTSS 1725

Qy      662 AAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKSVPEHAELVEDSSPESEP 721
      | | | :| :| | | | :| :| :| :| :| :| :| :|
Db      1726 AHTPS-----QIASPLQEDTLSDVPPRDMSLYASLASEKVQSLEGEKL----SPKSDI 1775

Qy      722 VDLFSDDSIPEVPQTQEEAVMLMKESLTVSETVAQHKEERLSASPQELGKPYL-ESFQP 780
      | :| | :| :| | | | :| :| :| :| :| :| :| :|
Db      1776 SPLTPRESSPTYSPGFSDSTSGAKES-TAAYQTSSSPPIDAAAAEPYGRSSMLFDTMQH 1834

Qy      781 NLHSTKDAASNDIPTLTKEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIE 840
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      1835 HLALSRDLTTSSV----EKDNGGKTPGDFNYAYQKPESTTESPDEEDYDYE--SHEKTIQ 1888

Qy      841 IIDEFPPTFVSAKDDSPK----LAKEYTDLEVSDKSEIANIQSGADSLPCLELPCDLSFKN 896
      | : :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      1889 AHDVGGYGYEKTERTIKSPCDSGYSYETIEKTTKTP----EDGGYS-----CEITEKT 1937

Qy      897 IYPKDEVHVSDEFSENRRSSVSKAS-----ISPSNVSALEPQTEMGSIVKSKSL 944
      :| | | | : :| :| :| :| :| :| :| :| :|
Db      1938 TRTPEEGGYSYEISEKTTTRTPEVSGYTYEKTERRRLDDISNGYDDTEDGGHTLGDCSY 1997

Qy      945 TKEAEKKLPSDTEKEDRS 962
      : | :| :| | | |
Db      1998 SYETTEKITSFPESESYS 2015

```

RESULT 14

MAPB_HUMAN

```

ID   MAPB_HUMAN          STANDARD;          PRT;   2468 AA.
AC   P46821;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain
DE   LC1].
GN   MAP1B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=95104835; PubMed=7806212;
 RA Lien L.L., Feener C., Fischbach N., Kunkel L.M.;
 RT "Cloning of human microtubule-associated protein 1B and the
 RT identification of a related gene on chromosome 15.";
 RL Genomics 22:273-280(1994).
 CC -!- FUNCTION: The function of brain MAPS is essentially unknown.
 CC Phosphorylated MAP1B may play a role in the cytoskeletal changes
 CC that accompany neurite extension. Possibly MAP1B Binds to at least
 CC two tubulin subunits in the polymer, and this bridging of subunits
 CC might be involved in nucleating microtubule polymerization and in
 CC stabilizing microtubules.
 CC -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
 CC with MAP1A and MAP1B proteins.
 CC -!- DOMAIN: Has a highly basic region with many copies of the sequence
 CC KKEE and KKEI/V, repeated but not at fixed intervals, which is
 CC responsible for the binding of MAP1B to microtubules.
 CC -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
 CC from MAP1B by proteolytic processing. It is free to associate with
 CC both MAP1A and MAP1B. It interacts with the amino-terminal region
 CC of MAP1B (By similarity).
 CC -!- SIMILARITY: TO MAP1A.
 CC -----
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 CC -----
 DR EMBL; L06237; AAA18904.1; -.
 DR Genew; HGNC:6836; MAP1B.
 DR MIM; 157129; -.
 DR GO; GO:0005875; C:microtubule associated complex; TAS.
 DR InterPro; IPR000102; MAP1B_neuraxin.
 DR Pfam; PF00414; MAP1B_neuraxin; 10.
 DR PROSITE; PS00230; MAP1B_NEURAXIN; 6.
 KW Microtubule; Repeat; Phosphorylation.
 FT CHAIN ? 2468 MAP1 LIGHT CHAIN LC1.
 FT REPEAT 1878 1894 MAP1B 1.
 FT REPEAT 1895 1911 MAP1B 2.
 FT REPEAT 1912 1928 MAP1B 3.
 FT REPEAT 1929 1945 MAP1B 4.
 FT REPEAT 1946 1962 MAP1B 5.
 FT REPEAT 1963 1979 MAP1B 6.
 FT REPEAT 1997 2013 MAP1B 7.
 FT REPEAT 2014 2030 MAP1B 8.
 FT REPEAT 2031 2047 MAP1B 9.
 FT REPEAT 2048 2064 MAP1B 10.
 FT DOMAIN 589 790 LYS-RICH (HIGHLY BASIC, CONTAINS MANY
 FT KKEE AND KKEI/V REPEATS).
 SQ SEQUENCE 2468 AA; 270618 MW; 540839CBDF09D461 CRC64;

Query Match 4.9%; Score 288; DB 1; Length 2468;
 Best Local Similarity 20.2%; Pred. No. 0.0017;
 Matches 251; Conservative 166; Mismatches 441; Indels 386; Gaps 56;

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Qy      13 STDSPPR--PPPAFKYQFVTEPEDEEDEEE-----EED-----EEEDDED 50
      :|| |: | : :|||::||| :|| || |
Db      625 ATDVKPKAAKEKTVKKETKVKPEDKKEEKEKPKKEVAKKEDKTPIKKEEKPKKEEVKKEV 684

Qy      51 LEELEVLERKPAAGLSAAAVPPAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWER 110
      :|:: |:| | : : : : : : : :|:
Db      685 KKEIKKEEKK-----EPKKEVKKETPPKEVKKEVKKEEKKEVKKE---EK 726

Qy     111 SPAAPAPSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAEPAAPSTPAAPKRRG-- 168
      | || | : || :|| | | | : | || :|
Db     727 EPKKEIKKLPKDAKKSSTPLSEAKKPAALKPKVPKKEESVKKDSVA----AGKPKEKGKI 782

Qy     169 -----SGSVDETLFAL-----PA-----ASEPVIPSSAEKIMDLME 199
      | | :| | | :| | :| | |
Db     783 KVIKKEGKAAEAVAAVGTGATTAAVMAAAGIAAIGPAKELEAERSLMSSPEDLT KD FEE 842

Qy     200 QPGNTVSSGQEDFPSV--LLETAASLPSLSPLSTVSFKEHGYLGNL SAVSSSEG TIEETLN 258
      | : :| :|:| | | : : : | | || | |
Db     843 LKAE EVDVTKDIKPQLELIEDEEKLKETEPVEAYVIQKEREVTKGPAESPDEG-ITTEG 901

Qy     259 EASKELPERATNPFVNRDLAEFSELEYSEMGS SFKGS PKGESAILVENTK--EEVIVRSKD 317
      | | | : : : :| :|:|:| | : | : || :|
Db     902 EGECEQTPEELEPVEKQGVDDIEKFE--DEGAGFEES--SETGDYEEKAE TEEAEEPEED 957

Qy     318 KEDLVC--SAALHSP-----QESPVGKEDRVVSPEKTM DIFNEMQMSV 358
      |: || ||: ||| :|| :|| |: || |
Db     958 GEEHVCVSASKHSPTED EESAKAEADAYIREKRESVASGDDRA---EEDMD---EAIEKG 1011

Qy     359 VAPVREEYADFKPF EQAWEVK-DTYEGSRDVL AARANVESKVD RK CLEDSLEQ----- 410
      | || || : :| : : : || : : | | : ||: | :
Db    1012 EAEQSEEEADEE--DKAEDAREEEYEPEK--MEAEDYVMAVVDKAAEAGGAE EQY GFLT T 1067

Qy     411 --KSLGKDSEGR-----NEDASFPSTPEPVKDSSRAYITCASFTSATESTT 454
      | || | || :| : | | :| : : :| :| :
Db    1068 PTKQLGAQSPGREPASSIHDETLPGGSESEATASDEENREDQPEEFTATSGYTQSTIEIS 1127

Qy     455 ANTFPL-----LEDHTSENKTDEK-----KIEERKAQIITEKTS-PKTSNPFLVAV 499
      : |: : | |: :|: | : : : : :| | |
Db    1128 SEPTPMDEMSTPRDVMSDET NNEETESPSQEFVNITKYESSLYSQEYSKPADVTPLNGFS 1187

Qy     500 QDSEADYVTTDTLSKVTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDL--- 556
      : |: | || |: : | : | : | | :| : :| :|:
Db    1188 EGSKTD--ATDGKDYNASASTISPPSSMEED---KFSRSALRDAYCSEVKASTTLDIKDS 1242

Qy     557 --VQTSEAIQESLYPTAQLCP-----SFE-----EAEATPSPVLPDIV 592
      :|| : | |: | :| :| ||| :|| |: :
Db    1243 ISAVSSEKVS PSKSPSLSPSPSPLEKTPLGERSVNFSLTPNEIKVSAEAEVAPVSPEVT 1302

Qy     593 ME-----APLNSLLPSAG-----ASVVQ----- 610
      | :| |: || | :|
Db    1303 QEVVEEH CASPEDKTLEVVS PSQSVTGSAGHTPYYSPTDEKSSHLPTEVIEKPPAVPVS 1362

Qy     611 -----PSVSPLEAPPPVSYDSIK--LEPENPPP-----YEEAMNVALKALG 649

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      |||:: | | | | : | | | | | : : | | |
Db      1363 FEFSDAKDENERASVSPMDEVPDSESPIEKVLSPLRSPPLIGSESAYESFLSADDKASG 1422
Qy      650 TKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPD-FSNYSEIA-----KF 701
      : |:: | | : || | | : |
Db      1423 -----RGAESPF-----EEKSGKQGSPDQVSPVSEMTSTSLYQDKQ 1458
Qy      702 EKSVPHEAELVEDSSPE-----SEPVDLFSDDSIPEVPQTQ-----EEAV 741
      | : | : | | | | : | : : | | | :
Db      1459 EKGSTDFAPIKEDFGQEKKTDDVEAMSSQPALALDERKLGDVSPQTQIDVSQFGSFKEDTK 1518
Qy      742 MLMKE-----SLTEVSETVAQ----HKEERLSASPQELG-----KPYLESFQPNLHSTK 786
      | : | | | | | : | | | : : | : | : |
Db      1519 MSISEGTVSDKSATPVDEGVAEDTYSHMEGVASVSTASVATSSFEPTTDDVSPSLH--- 1575
Qy      787 DAASNDIPTLTK-KEKISLQMEEFNTAIYSNDDLSSKEDKIKESETFSDSSPIEIIDEF 845
      | | | : : : : | : : : | | :
Db      1576 --AEVGSPHSTEVDDSLSVSVVQTPPT-FQETEMSPSKEECPR----- 1615
Qy      846 PTFVSAKDDSPKLAKEYTDLE--VSDKSEIANIQSGADSLPCLELPCDLSFKN----- 896
      | : | | | | | : | : | : : | : | | :
Db      1616 PMSISPPDFSPKTAKSRTPVQDHRSEQSSM-SIEFGQES-PEQSLAMDFSRQSPDHPTVG 1673
Qy      897 -----IYPKDE-VHVSDEFSENRSSVSKASISPSNV 926
      | | : | : | | : | |
Db      1674 AGVLHITENGPTVDYSPSDMQDSSLSHKIPMEEPSYTDNDLSELISVSQVEASPSTS 1733
Qy      927 SALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAE 970
      || | : : | : : | : | | | : : |
Db      1734 SAHTP-SQIASPLQEDTLSDVAPPR-----DMSLYASILTSE 1768

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RESULT 15

MAPB_MOUSE

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ID MAPB_MOUSE STANDARD; PRT; 2464 AA.
AC P14873;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))
DE [Contains: MAP1 light chain LC1].
GN MAP1B OR MTAP1B OR MTAP5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND DOMAIN.
RC STRAIN=Swiss Webster; TISSUE=Brain;
RX MEDLINE=90094539; PubMed=2480963;
RA Noble M., Lewis S.A., Cowan N.J.;
RT "The microtubule binding domain of microtubule-associated protein
RT MAP1B contains a repeated sequence motif unrelated to that of MAP2
RT and tau.";
RL J. Cell Biol. 109:3367-3376(1989).
CC -!- FUNCTION: The function of brain MAPS is essentially unknown.
CC Phosphorylated MAP1B may play a role in the cytoskeletal changes

```

CC that accompany neurite extension. Possibly MAP1B Binds to at least
 CC two tubulin subunits in the polymer, and this bridging of subunits
 CC might be involved in nucleating microtubule polymerization and in
 CC stabilizing microtubules.
 CC -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
 CC with MAP1A and MAP1B proteins.
 CC -!- DOMAIN: Has a highly basic region with many copies of the sequence
 CC KKEE and KKEI/V, repeated but not at fixed intervals, which is
 CC responsible for the binding of MAP1B to microtubules.
 CC -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
 CC from MAP1B by proteolytic processing. It is free to associate with
 CC both MAP1A and MAP1B. It interacts with the amino-terminal region
 CC of MAP1B.
 CC -!- SIMILARITY: TO MAP1A.

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DR EMBL; X51396; CAA35761.1; -.
 DR PIR; S07549; QRMSP1.
 DR MGD; MGI:1306778; Mtap1b.
 DR GO; GO:0016358; P:dendrite morphogenesis; IMP.
 DR GO; GO:0001578; P:microtubule bundling; IMP.
 DR InterPro; IPR000102; MAP1B_neuraxin.
 DR Pfam; PF00414; MAP1B_neuraxin; 10.
 DR PROSITE; PS00230; MAP1B_NEURAXIN; 7.
 KW Microtubule; Repeat; Phosphorylation.

FT CHAIN ? 2464 MAP1 LIGHT CHAIN LC1.
 FT REPEAT 1874 1890 MAP1B 1.
 FT REPEAT 1891 1907 MAP1B 2.
 FT REPEAT 1908 1924 MAP1B 3.
 FT REPEAT 1925 1941 MAP1B 4.
 FT REPEAT 1942 1958 MAP1B 5.
 FT REPEAT 1959 1975 MAP1B 6.
 FT REPEAT 1993 2009 MAP1B 7.
 FT REPEAT 2010 2026 MAP1B 8.
 FT REPEAT 2027 2043 MAP1B 9.
 FT REPEAT 2044 2060 MAP1B 10.
 FT DOMAIN 589 787 LYS-RICH (HIGHLY BASIC, CONTAINS MANY
 FT KKEE AND KKEI/V REPEATS).
 SQ SEQUENCE 2464 AA; 270408 MW; FBD3DD99CFDBDA87 CRC64;

Query Match 4.9%; Score 284; DB 1; Length 2464;
 Best Local Similarity 20.7%; Pred. No. 0.0025;
 Matches 233; Conservative 159; Mismatches 424; Indels 312; Gaps 51;

QY 31 EPEDEEDEEEEEDEEED-----DEDLEEE-----VLERKPAAG-----LSAAAVP 71
 | | | : | | | | : | | | | : | | | : |
 Db 1009 EAEQSEEEGEEEDKAEDAREEGYEPDKTEAEDYVMAVADKAAEAGVTEEQYGYLGTS AKQ 1068
 QY 72 PAAAPLLDFSS-----DSVPPAPRGPLPAAPPAAPERQP-----SWERSPAAPA 116
 | : | : : | : : | | : | | : |

Db	1069	PGIQSPSPREPASSIHDETLPGGSESEATASDEENREDQPPEFTATSGYTQSTIEISSEPT	1128
Qy	117	P---SLPPAAAVLPSKLPEDDEPPARP-----PPPPPAGASPLAEP--	155
Db	1129	PMDEMSTPRDVMSETNNEETESPSQEFVNITKYESSLYSQEYSKPAVASFNGLSEGSKT	1188
Qy	156	-----APPSTPAAPKRRGSGSVDETLEFALPA-----ASEPVIPISSAEKIMDLMEQ	200
Db	1189	DATDGKDYNASASTISPP-----SSMEEDKFSKSALRDAYCSEEKELKASAE--LDIKDV	1241
Qy	201	PGNTVSSGQEDFPSVLLETAASLPSLSPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEA	260
Db	1242	SDERLS-----PAKSPSLSP-----SPPSPIEKT----	1265
Qy	261	SKELPERATNPFVNRDLAEFS-----ELEYSEMSSFKGSPKGESAILVEN--TKEEVIVR	314
Db	1266	--PLGERSVN-----FSLTPNEIKVSAEGEARSVSPGVTQAVVEEHCASPEEKTLE	1314
Qy	315	SKDKEDLVCSAALHSP--QESPVGKEDRVVSPEKTMDFNEMQMSVVA--PVREEYADFK--	370
Db	1315	VVSPSQSVTGSAGHTPPYQSP-----TDEKSSHLPTEVSENAQAVPVSFEFSEAKDE	1366
Qy	371	-----PFEQAWEVKDTYEGSRDVLAAARANVESKVDRKCLED--SLEQKSLGKDS----	417
Db	1367	NERASLSPMDE--PVPDSESPVEKVLSPLRSPPLLGSESPVEDFLSADSKVLGRRESPEF	1424
Qy	418	EGRNEDASFPSTPEPVKDSSRAYITCASFTSATESTTANTFPLLEDHTSENKT-----	470
Db	1425	EGKNGKQGFPDRESPVSDLT----STGLYQDKQEEKSTGFIPIKEDFGPEKKTSDVETMS	1480
Qy	471	-----DEKKI-----EERKAQIITEKTSPKTSNPFLVAVQDSEAD	505
Db	1481	SQSALALDERKLGGDVSPQTQIDVSQFGSFKEDTKMSISEGTVSDKSATPVDEGV--AEDT	1538
Qy	506	YVTTDTLSKVTEAAV--SNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAI	563
Db	1539	YSHMEGVASVSTASVATSSFPPEPTDD--VSPSLHAEVGSHPSTEVDDSLSVSVVQTPPTF	1597
Qy	564	QES--LYPTAQLCP---SFEEAEATP-----SPVLPDIVMEAPLNSLL--	601
Db	1598	QETEMSPSKEECPRPMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSFAMD	1657
Qy	602	-----PSAGASVVQPSVSPLEAPPVSYD-----SIKLEPENPPPYEEAMNVA	644
Db	1658	FSRQSPDHPTLGASVLHITEN---GPTEVDYSPCDIQDSSLSHKIPTEEPSYTQDNDLS	1714
Qy	645	LKALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSPDFSNYSEIAKFEKS	704
Db	1715	--ELISVSQVEASPSTSSAHTPS-----QIASPLQEDTLSDVPPPREMSLYASLA-----	1762
Qy	705	VPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVML---MKESLTVSETVAQHKE	760
Db	1763	----SEKVQ--SLEGEKLSPKSDIS----PLTPRESSPLYSPGFSDDTSAAKETAAAH--	1810
Qy	761	ERLSASP---QELGKPY-----LESFQPNLHSTKDAASNDIPTLTKEKISLQMEEFN	810
Db	1811	--QASSPPIDAATAEPYGFRRSMLFDTMOHHLALNRDLTTSSV----EKDSGGKTPGDFN	1865

Qy 811 TAIYSNDDLSSKEDKIKESETFSDSSPIEIIIDEFPTFVSAKDDSPK----LAKEYTDLE 866
 | :: | ::: : | | | : : : | : |
 Db 1866 YAYQKPENAAGSPDEEDYDYE--SQEKTIRTHDVVRYYYEKTERTIKSPCDSGYSYETIE 1923

Qy 867 VSDKSEIANIQSGADSLPCLELPCDLSFKNIYPKDEVHVSDEFSENRSSVSKAS----- 920
 : | : : | | : : | : | : | : : |
 Db 1924 KTTKTP----EDGG-----YTCEITEKTTRTPEEGGYSYEISEKTTRTPEVSGYTYEK 1972

Qy 921 -----ISPSNVSALEPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRS 962
 : : : : | : | : | : | : | : |
 Db 1973 TERSRRLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSFPESESYS 2020

Search completed: September 3, 2004, 16:06:02
 Job time : 25.4629 secs